us-09-107-979-4.rai

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                                                                             November 2, 2004, 13:19:25; Search time 38 Seconds (without alignments) 82.025 Million cell updates/sec
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Sequence 3, Ar
Sequence 3, Ar
Sequence 23, A
Sequence 2, Ap
Sequence 2, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, 1
Sequence 8, 1
Sequence 4, 1
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Sequence 1,
Sequence 14,
Sequence 14,
Sequence 12,
Sequence 3,
Sequence 3,
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Sequence 6,
Sequence 2,
Sequence 7,
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Sequence 6
Sequence 2
Sequence 1
                                                                                                                                   US-09-107-979-4
277
1 HFKPCRDKDLAYCLNDGBCF.....SHKHCRCKEGYQGVRCDQFL
                                                                                                                                                                                                                                                          478139
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1. /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2. /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

3. /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/BCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-899-437-8

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US-09-553-769-6

US-09-553-769-6

US-09-097-681-2

US-08-899-437-3

US-08-899-437-3

US-08-899-437-2

US-08-899-437-2

US-08-899-437-2

US-08-899-437-2

US-08-899-437-2

US-08-999-437-2

US-08-999-437-6

US-08-999-437-6

US-08-126-121-6

US-08-126-121-6

US-08-126-121-6

US-08-126-121-6

US-08-126-121-6

US-08-126-121-1

US-08-126-121-14
                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                               478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                    - protein search, using sw model
                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                   Perfect score:
                                                     OM protein
                                                                                                                                                                                                                                                                                                                                                                                   Database :
                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                 Sequence:
                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Result
                                                                                                                                   Title:
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Sequence 3, Appli Sequence 17, Appl Sequence 111, Appl Sequence 62, Appl Sequence 221, Appl Sequence 221, Appl Sequence 55, Appl Sequence 55, Appl Sequence 136, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 2, Appli Sequence 2, Appli	Rose, Zhang, Dong Xiao Neuregulin Related Or Sk	Length 47; Indels 0; Gaps 0; VRCDQFL 47
2 US-08-761-038-3 4 US-09-097-681-17 1 US-08-179-481-111 1 US-08-341-018-62 3 US-08-470-335-221 3 US-08-470-335-221 4 US-08-471-295F-55 4 US-08-411-295F-56 4 US-08-411-295F-98 4 US-08-411-295F-136 4 US-08-411-295F-136 1 US-08-456-211-10 1 US-08-456-21-10 2 US-08-456-21-10 3 US-08-101-544-2 5 PCT-US92-04295A-10 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016 3 US-08-341-016	Melanie Specific ss Theref	Main/amino acid seq. Score 277; DB 3; Pred. No. 2.9e-26; ; Mismatches 0; VIETLTGSHKHCRCKEGYQG
113.5 41.0 52 113.5 41.0 53 113.5 41.0 63 113.5 41.0 63 113.5 41.0 63 113.5 41.0 63 113.5 41.0 65 113.5 41.0 66 113.5 41.0 66	437-4 4, Application o. 6121415 CANT. Godowski, OF INVENTION: OF INVENTION: OF INVENTION: OF SEQUENCES: SERONDEES: SERONDES: SOUTH MAN WAY TYPE: ORALICATION ORALICATION: NEY APPLICATION: NEY APPLICATION: NEY APPLICATION: NEY APPLICATION: NEY APPLICATION: SERENCEST NUMBER: SERENCE	ப்பிங்பிய வு
8 9 9 9 1 2 2 3 3 3 3 3 3 3 2 2 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	RESULT 1 US-08-899-437-4 Sequence 4, A Sequence 6 Sequence 6 COMPRY: STAE:) NAME/KO) LOCATION) TOBNYII) OTHER US-08-899-437 Query Match Best Local Matches 4

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TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-126-121-4
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                                                                                                        Sequence 8, Application US/08899437

Patent No. 6121415

GENERAL INFORMATION:
GENERAL OF DATE:
GENERAL OF DATE:
GENERAL OF DATE:
GOGOWSKI, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION:
ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION:
Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09126121

Patent No. 6252051

CENERAL INFORMATION:
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATE:
APPLICATION DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CONICY, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 91084R1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 277; DB 3; Best Local Similarity 100.0%; Pred. No. 2.9e-26; Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: NRG3 EGF-like domain/amino acid seq
                                                                                                                                                                                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 47 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                              94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
TELEFAX: 6
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                                                                                          US-08-899-437-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-899-437-8
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RESULT 4
US-09-126-121-8
; Sequence 8, Application US/09126121
; Partent No. 6252051
; GENERAL INFORMATION:
; APPLICANT: Gedowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
; CORRESPONDENCE 23
; CORRESPONDENCE Generatech, Inc. STREET: 1 DNA May
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; IP: 94080
; TIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: NRG3 EGF-like domain/amino acid seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
100.0%; Score 277; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OSTWARE: WinhPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
APPLICATION NUMBER: US/09/126,121
APLICATION NUMBER: 30-Jul-1998
CLASSIFICATION:
NAME: Conley, Delicare L.
REGISTRATION NUMBER: 36,487
REGISTRATION NUMBER: 36,487
REGISTRATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION: NUMBER: PLOSARIDI
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COBRATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/126,121 FLING CLASSIFICATION:
                                                                                                                                                                                                                                                                           P1084R1D1
                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: CONLEY, DEITGTE L.
REGISTRATION UNDBER: 36,487
REFERENCE/DOCKET NUMBER: P1084
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-2066
TELEPAX: 650/252-2066
TELEPAX: 650/252-2066
TELEPAX: 650/252-2066
TELEPAX: 47 amino acids
TENGTH: 47 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 650/225-2066
650/952-9881
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: Amino Acid
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco
STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ..
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                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 277; DB 4; Length 157; 100.0%; Pred. No. 9.8e-26; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: hNRG3 extracellular domain/Amino AcidSeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CHASSIFICATION: 435
US 60/049,942
                                                                                                                  PF383PCT
                 FILING DATE: 17-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: HOOVEY, KENLEY K.
REGISTRATION NUMBER: 40,302
REFERENCE/DOCKET NUMBER: PF383
TELECOMUNICATION INFORMATION:
TELEPHONE: 301-309-8439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 157 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/08899437; Patent No. 6121415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: PI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 650/225-2066
650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : 360 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 650/225-2060
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 incl
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94080
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US-08-899-437-7
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                                                                                                                                                                                                                                                                                                                                                                                                       CEQUENCE (Application US/09553769)

Patent No. 6544759

GENERAL INFORMATION:
APPLICANT: Harrari, Daniel
APPLICANT: Yarden, Yosef
TITLE OF INVENTION: SEQUENCES ENCODING SAME AND USES THEREOF
TITLE OF INVENTION NUMBER: US/09/553,769
CURRENT APPLICATION NUMBER: US/09/553,769
CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.0
SEQ ID NO 6
LENGTH: 48
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                                                                                                                                                                Length 47;
                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,681
                     NAME/KEY: NRG3 EGF-like domain/amino acid seq.
                                                                                                                                                           Query Match
100.0%; Score 277; DB 3;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 277; DB 4;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Young, Paul
APPLICANT: King, C. Richter
APPLICANT: Hijazi, Mai
APPLICANT: Ruben, Steve
TITLE OF INVENTION: Heregulin-Like Factor
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09097681 Patent No. 6727077 GENERAL INFORMATION:
                                         LOCATION: 1-47

LOCATION: 1-47

IDENTIFICATION METHOD:

OCHER INFORMATION:

US-09-126-121-8
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Mus musculus
US-09-553-769-6
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US-09-553-769-6
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US-09-097-681-2
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US-08-899-437-3
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                                                                                                                                                             Sequence 7, Application US/09126121
Patent No. 6252051
GENERAL INFORMATION:
APPLICANT: Gadowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South Asan Francisco
STATE: California
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                                   286 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 332
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  1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: BP C compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: CONLey, Deirdre L.
REGISTATION UNDRER: 36,487
REFERENCE/DOCKET NUMBER: P1084RID1
TELECOMMUNICATION INFORMATION:
TELEFRAN: 650/252-2066
TELEFRAN: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Matches 47; Conservative
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IDENTIFICATION METHOD:
OTHER INFORMATION:
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US-08-899-437-3
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Gaps
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Sequence 3, Application US/09126121

Sequence 3, Application US/09126121

Patent No. 652051

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related

TITLE OF INVENTION: Ligands and Uses Therefor

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 362;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 277; DB 3;
100.0%; Pred. No. 2.3e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 18M PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                SOFTWARE: Winbatin (Genetical)
SOFTWARE: Winbatin (Genetical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Unl-1997
CLASSIFICATION: 435
ATTORNEY/GENT INFORMATION:
NAME: Conley, Delirdre L.
REGISTRATION NUMBER: 36,487
REFERNICE/DOCKET NUMBER: P1084R1
TELEPHONE: 650/25-2066
TELEPHONE: 650/25-2066
TELEPHONE: 650/25-2066
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGRATION FOR SEQ ID NO: 3:
LENGRATION ACID ACID SEG ID NO: 3:
TELEPHONE: AMINO ACID SEG ID NO: 3:
TELEPHONE: AMINO ACID SEG ID NO: 3:
TELEPHONE: AMINO ACID SEG ID NO: 3:
TOPOLOGY: Linear
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NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 47; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 1-362
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94080
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94080
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US-09-126-121-23
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US-08-899-437-2
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                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 23, Application US/08899437

Patent No. 6121415

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
ADDRESSEB: Genentech, Inc.
STREET: 1 DNA Way
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                                                                                                                                                                                                  Length 362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
100.0%; Score 277; DB 3; Length 696;
Best Local Similarity 100.0%; Pred. No. 4.5e-25;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                            1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                              NAME/KEY: mNRG3 extracellular domainAmino acid seq
                                                                                                                                                                                              100.0%; Score 277; DB 3;
100.0%; Pred. No. 2.3e-25;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1EM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: COLLEY, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: PLOB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , DENTIFICATION METHOD:

, OTHER INFORMATION:
US-08-899-437-23
362 amino acids
Amino Acid
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650/952-9881
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Amino Acid
                                                                                                                                                                                                                Local Similarity 100.
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                                                                                               LOCATION: 1-362
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                     TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
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                                                                                                                                            ;
US-09-126-121-3
  LENGTH:
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Matches
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RESULT 12

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                                                                        APPLICATE: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DAW Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
NUMBER OF SEQUENCES: 23
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
FILLING DATE: 30-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 23, Application US/09126121
Patent No. 6252051
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 696 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NRG3B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 1-696
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION:
US-09-126-121-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: Linear FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE:
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
                                                                                                                                                                               47; Conservative
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IDENTIFICATION METHOD:
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US-08-899-437-6
; OTHER INFORMATION:
US-09-126-121-2
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FEATURE:
NAME/KEY: hNRG3B1
                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
US-08-899-437-6
                                                                                                            Query Match
                                                                                                                                                                               Matches
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US-09-126-121-2
; Sequence 2, Application US/09126121
; Patent No. 6282051
; GENERAL INFORMATION:
; APPLICATT GOOGNSKI, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
; TITLE OF INVENTION: Ligands and Uses Therefor
; NUMBER FOR SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genented, Inc.
; STREET: 1 DAW Way
; CITY: South San Francisco
; STAREY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 277; DB 3; Length 713; 1 Similarity 100.0%; Pred. No. 4.7e-25; 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               288 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
LOCATION: 1-713
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Mouse NRG3 (mNRG3)/amino acid seq.
LOCATION: 1-713
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-U11-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                         P1084R1
                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084
TELECOMMUNICATION INPORMATION:
TELEPAX: 650/225-206
TELEFAX: 650/925-9881
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 amino acids
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CTHER INFORMATION:
US-08-899-437-2
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MEDIUM TYPE: 3.5 inch
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Best Local Similarity
Matches 47; Conserv
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Sequence 6, Application US/08899437

Patent No. 6121415

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICARN: Gedowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.
STREET: 1 DAA WAY
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Length 713;
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100.0%; Pred. No. 4.7e-25;
iive 0; Mismatches 0;
     100.0%; Score 277; DB 3; 100.0%; Pred. No. 4.7e-25;
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1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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sequence 23, Appl Sequence 23, Appl Sequence 2, Appl Sequence 2, Appl Sequence 6, Appl Sequence 19, Appl Sequence 19, Appl Sequence 18, Appl Sequence 315, Appl Seque
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Sequence 8, Appli
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                                                                                                                                                                    November 2, 2004, 13:37:16; Search time 38 Seconds (without alignments) 82.025 Million cell updates/sec
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('GGTZ 6'fptdata1/iaa/5A COMB.pep:*

('GGTZ 6'fptdata1/iaa/6A COMB.pep:*

('GGTZ 6'fptdata1/iaa/6A COMB.pep:*

('GGTZ 6'fptdata1/iaa/6B COMB.pep:*

('GGTZ 6'fptdata1/iaa/6B COMB.pep:*

('GGTZ 6'fptdata1/iaa/PCTUS COMB.pep:*

('GGTZ 6'fptdata1/iaa/backfiles1.pep:*
                       GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-905-125A-315
US-09-902-775A-315
US-09-906-700-315
US-09-903-603A-315
US-09-134-001C-4939
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US-09-126-121-3
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US-09-126-121-23
US-09-126-121-2
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US-09-126-121-6
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US-08-099-437-12
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US-09-465-558-70
US-09-465-558-68
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US-09-097-681-2
US-08-899-437-7
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                                                                                                                     - protein search, using sw model
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Maximum DB seq length: 200000000
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880, App
340, App
1328, Ap
20665, A
6117, Ap
13463, Ap
13463, Ap
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8, Appli
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Patent No. 6121415

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: Ligands and Uses Therefor
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCE: 23
CORRESPONDENCE ADDRES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
CONNERY: USA
                                                                                                                                Sequence Seq
                                  Sequence
Sequence
Sequence
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US-09-538-092-691

US-09-270-767-42448

US-09-205-258-904

US-09-198-452A-880

US-09-1184-452A-880

US-09-1184-6210-3403

US-09-710-279-696

US-09-710-279-696

US-09-710-279-665

US-09-710-279-1328

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US-09-710-279-1328

US-09-710-279-1328

US-09-710-279-1328

US-09-710-732A-6507

US-09-489-032A-13463

US-09-328-352-7421

US-09-875-883A-8

US-09-875-883A-8

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US-09-875-883A-8
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LOCATION: 1-47
IDENTIFICATION METHOD:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disconputER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WINPERIN (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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REGISTRATION NUMBER: 36,487
REPRENCE/DOCKET NUMBER: P1084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 47; Conservative
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Sequence 8, Application US/08899437

Parent No. 6121415

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: LDAM WAY
CITY: South San Francisco
STATE: California
COUVENTY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Batent No. 6252051

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPES 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFFANTING SYSTEM: PC-DOS/MS-DOS SOFFANTION DATA: APPLICATION NATE: US/08/899,437 FILING DATE: 24-Jul-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: CONICY, Deirdre L. REALSTRATION NUMBER: 36,487 REFERENCE/DOCKET NUMBER: 91084R1 TELECOMMUICATION INFORMATION: TELECOMMUICATION INFORMATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION INFORMATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION: TELECOMMUICATION INFORMATION: TELECOMMUICATION: TELECOMMUICATION
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 47 amino acids TVPE: Amino Acid TVPE: Amino Acid
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Best Local Similarity 100.0
Matches 47; Conservative
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, IDENTIFICATION METHOD: ;

, OTHER INFORMATION: US-08-899-437-8
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ZIP: 94080
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Gaps
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Patent No. 6252051
GENERAL INPORMATION:
APPLICANT: GOOWSKI, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA May
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 47; DB 3; Length 47; 100.0%; Pred. No. 4.9e-44; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: NRG3 EGF-like domain/amino acid seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTER READBLE FORM:
COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
TTING DATE: 30-Jul-1998
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURENT APPLICATION DATA: APPLICATION NUMBER: US/09/126,121 FILING DATE: 30-Jul-1998
                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COALGAY, DGITATE L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
TELECHONIS: 650/225-2066
TELEFAX: 650/252-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 30-Jul-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: COLLEY, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/POCKET NUMBER: P1084RID1
TELEPHONE: 650/225-2066
                                                                                                            UMBER: US/09/126,121
30-Jul-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 47 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0
.....hes 47; Conservative
                                                                                                                                                                                                                                                                                                                             TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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LENGTH: 47 amino acids
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1-47
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: Amino Acid
TOPOLOGY: Linear
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Patent No. 6121415
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genethech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 47; DB 4; Length 157; 100.0%; Pred. No. 1.4e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
US 60/049,942
                                                                                                              PF383PCT
                                                        REGISTRATION NUMBER: 40,302
REGISTRATION NUMBER: 40,302
REFRENCE/DOCKET NUMBER: PF38
TELECOMMUNICATION INFORNATION:
TELEFAX: 301-309-804
INPORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1(
TELECOMMUNICATION INFORMATION:
                  FILING DATE: 17-JUN-1997 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Conley, Deirdre L
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 360 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                               47; Conservative
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Best Local Similarity 100.
Matches 47; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                LENGTH: 157 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: protein
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                     amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION
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Betent No. 6544759

GENERAL INFORMATION:
APPLICANT: Harari, Daniel
APPLICANT: Yarden, Yosel
TITLE OF INVENTION: NOVEL GROWTH FACTOR WHICH ACTS THROUGH ErbB-4 RECEPTOR TYROSINE K
TITLE OF INVENTION: SEQUENCES ENCODING SAME AND USES THEREOF
FILE REFERENCE: 00/20522
CURRENT PAPLICATION NUMBER: US/09/553,769
CURRENT FILING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 18
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                                                                                                                                                       Score 47; DB 3; Length 47; Pred. No. 4.9e-44;
                                                                                                                                                                                                   0; Indels
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ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,681
                     NAME/KEY: NRG3 EGF-like domain/amino acid seg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09097681

Sequence 2, Application US/09097681

Patent No. 6727077

GENERAL INFORMATION:
APPLICANT: Young, Paul
APPLICANT: King, C. Richter
APPLICANT: Hijazi, Mai
APPLICANT: Hijazi, Mai
APPLICANT: Riber, Steve
TITLE OF INVENTION: Heregulin-Like Factor
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: MD
                                                                                                                                                       Query Match
100.0%; Score 47; DB
Best Local Similarity 100.0%; Pred. No. 4.9
Matches 47; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.0
Matches 47; Conservative
                                        LOCATION: 1-47
IDENTIFICATION METHOD:
CTHER INFORMATION:
US-09-126-121-8
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US-09-553-769-6
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                                                                                                                                                                                                                                                                                                                                                                                  US-09-553-769-6
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COUNTRY:
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                                                                                                                                                                 US-09-126-121-7
Sequence 7, Application US/09126121
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ExbB Receptor-Specific Neurequlin Related TITLE OF INVENTION: Lagands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                o,
                                                  286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genetical)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-301-1998
CLASSIFICATION:
ATORNEY/AGENT INFORMATION:
NAME: COLLEY, Delirate L.
REGISTRATION NUMBER: 36,487
REFRENCE/DOCKET NUMBER: 91084R1D1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08899437
Patent No. 6121415
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 47; Conservative
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; OTHER INFORMATION:
US-09-126-121-7
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Gaps
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Sequence 3, Application US/09126121
Farent No. 6252051
FARENTAL INFORMATION:
APPLICANT:
APPLICANT:
CORRESPONDENCE:
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
COUNTRY: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: mNRG3 extracellular domainAmino acid seq
LOCATION: 1-362
             COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compactible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTOMAYOR: ABSTECATION: 435
ATTOMAYOR'S INFORMATION:
NAME: CONLEY, Deirdre L.
REGISTRATION UNBER: 36,487
REGISTRATION UNBER: 36,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: COnley, Delirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1D1
                                                                                                                                                                                                                                                                                                                                      REFERENCE DOCKET NUMBER: P106
TELECOMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/925-981
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 362 amino acids
TYPE: Amino Acid
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TELEPHONE: 650/225-2066
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: Linear
94080
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JS-09-126-121-23
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Sequence 23, Application US/08899437

Patent No. 6121415

GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
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                                                                                                                                                                                                                                   Query Match
100.0%; Score 47; DB 3; Length 362;
Best Local Similarity 100.0%; Pred. No. 3e-43;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                NAME/KEY: mNRG3 extracellular domainAmino acid seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 47; DB 3; I
Best Local Similarity 100.0%; Pred. No. 5.4e-43;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WinPatin (Genericeh)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,437
FILING DATE: 24-Unl-1997
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: COALGY, DEIGHE L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P108.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-2066
TELEPAK: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    696 amino acids
  : 362 amino acids
Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: Human NRG3B2
                                                                                                                                        ; IDENTIFICATION METHOD:
; OTHER INFORMATION:
US-09-126-121-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 1-696
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                         TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino Acid
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                                                                                                                            LOCATION:
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RESULT 12

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Jeannt No. 6121415

GENERAL INFORMATION:
APPLICANT: GGOWEN'S Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related TITLE OF INVENTION: Ligands and Uses Therefor NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: 3
CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
Sequence 23, Application US/09126121
Patent No. 6252051
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
TITLE OF INVENTION: Ligands and Uses Therefor
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 47; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 5.4e-43;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P1084R1D1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P106
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                         E: Genentech, Inc.
1 DNA Way
                                                                                                                                                                                                                   STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 696 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human NRG3B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1-696 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION:
US-09-126-121-23
                                                                                                                                                                                                                                                                                                                94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
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US-08-899-437-2
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: 720 amino acids
Amino Acid
                                                                                                       Best Local Similarity 100.
Matches 47; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 720 amino acid
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COTHER INFORMATION:

US-08-899-437-6
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  ; OTHER INFORMATION:
US-09-126-121-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: Amino Acid
TOPOLOGY: Linear
FEATURE:
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                                                                                    Query Match
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; Sequence 2, Application US/09126121
; Sequence 2, Application US/09126121
; Patent No. 6252051
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
; TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
; TITLE OF INVENTION: Ligands and Uses Therefor
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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100.0%; Score 47; DB 3; Length 713;
Best Local Similarity 100.0%; Pred. No. 5.5e-43;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
             APPLICATION UMBER: US/08/899,437
FILING DATE: 24-Jul-1997
CLASSIFICATION: 435
ATTORNAYAGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRACION NUMBER: 96,487
REFERENCE/DOCKET NUMBER: 91084R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/252-9681
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRATION POR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRATION POR AGI DI NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRATION AGI DI NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRATION AGI DI NO: 2:
SEQUENCE CHARACTERISTICS:
LENGRATION AGI DI NO: 2:
FRATURE: Amino Acid TOPOLOGY: Linear
FRATURE: Mouse NRG3 (mNRG3)/amino acid seq.
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ZIE: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 35 inch, 1.44 Mb floppy disk
COMPUTER: IDM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE MinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/126,121
FILING DATE: 30-Jul-1998
CLASSIFICATION: Deirdre L.
REGISTRATION NUMBER: 91084RID1
REGISTRATION NUMBER: 91084RID1
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEBRAX: 650/225-2066
TELEBRAX: 650/25-9881
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRACATERIFICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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TYPE: Amino Acid
TOPOLOGY: Linear
CURRENT APPLICATION DATA:
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DENTIFICATION METHOD:

CTHER INFORMATION:

US-08-899-437-2
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IDENTIFICATION METHOD:
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RESULT 15
US-08-899-437-6
i Sequence 6, Application US/08899437
patent No. 6121415
i GENERAL INFORMATION:
i APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: Ligands and Uses Therefor
i TITLE OF INVENTION: Ligands and Uses Therefor
i TITLE OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
i ADDRESSE: Genentech, Inc.
STREET: 1 DAA Way
CITY: South San Francisco
i STATE: California
COUNTRY: USA
                                                              Gaps
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                                                                                                                                                                       288 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 334
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Length 713;
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                                                                                                                    1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYOGVRCDOFL
100.0%; Score 47; DB 3; I
100.0%; Pred. No. 5.5e-43;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/899,437 FILING DATE: 24-Uul-1997 CLASSIFICATION: 4.35 ATTORNEY/AGENT INFORMATION: NAME: CONIEY, Deirdre L. REGISTRATION NUMBER: 36,487 REGISTRATION NUMBER: 36,487 REGISTRATION NUMBER: 36,487 REFERENCE/DOCKET NUMBER: 91084R1 TELECOMMUNICATION INPORMATION: TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: hNRG3B1 amino acid sequence
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Job time : 39 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, OM protein November 2, 2004, 13:10:39; Search time 157 Seconds (without alignments) 107.390 Million cell updates/sec Run on:

US-09-107-979-4 Title: Perfect score:

1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL 47 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

2002273 segs, 358729299 residues Searched:

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

A_Geneseq_23Sep04:* l: genesecn1980r:* Database

geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aaw97622 Human neu	Mouse	Human	Human	_	Aaw97621 Human neu		Abb08776 Human neu	Aaw97619 Human neu		Mouse	Mouse	Aaw97618 Human neu		Human	Human	Neu di	Aay69983 NDF/hered		Aaw05184 Neu diffe			EGF1.2		Human e
SUMMARIES		AAW97622	AAG66046	AAE36807	AAY05451	ADN48870	AAW97621	AAW97620	ABB08776	AAW97619	ABG32080	AAW97617	ABG32061	AAW97618	AAY05452	ABG32065	ADN48890	AAW05182	AAY69983	AAB12602	AAW05184	AAE36803	ADN48885	AAR55659	AAR46918	AAR67250
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ن	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	42	42	42.1	41.0	41.0	41.0	41.0	41.0	41.0
	Score	277	277	277	277	277	277	277	277	277	277	277	277	277	277	277	277	116.5	116.5		٠			113.5		113.5
	Result No.		7	3	4	ហ	9	7	σ,	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Aar96076 Epidermal	Aaw09363 EGFL2. 8/	Aar87461 Epidermal	Aab36702 EGF-like	Aar55663 EGFL6. 3/	Aar46922 EGFL6. 3/	Aar67254 Human epi	Aar96080 Epidermal	Aaw09367 EGFL6. 8/	Aar87465 Epidermal	Aar55662 EGFL5. 3/	Aar46921 EGFL5. 3/	Aar67253 Human epi	Aar96079 Epidermal	Aaw09366 EGFL5. 8/	Aar87464 Epidermal	Abj00043 Human neu	Abj00081 Human neu		
AAR96076	AAW09363	AAR87461	AAB36702	AAR55663	AAR46922	AAR67254	AAR96080	AAW09367	AAR87465	AAR55662	AAR46921	AAR67253	AAR96079	AAW09366	AAR87464	ABJ00043	ABJ00081	ADH77520	AAG67933
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63	63	63	99	83	83	83	83	83	83	88	88	88	88	88	88	99	66	66	101
41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0	41.0
113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5	113.5
26	27	78	59	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

AAW97622 standard; protein; 47 AA. (first entry) 10-MAY-1999 AAW97622; AAW97622

Human neuregulin related ligand NRG3 EGF-like domain.

Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.

Homo sapiens.

WO9902681-A1.

21-JAN-1999.

98WO-US013411. 30-JUN-1998;

97US-0052019P. 97US-00899437. 39-JUL-1997; 24-JUL-1997;

(GETH) GENENTECH INC.

Zhang D; Mark MR, Godowski PJ,

WPI; 1999-120882/10.

New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.

Claim 30; Page 64; 101pp; English.

This is the epidermal growth factor (EGF)-like domain of human neuregulin related ligand NRG3 (see also AAM97618), a novel member of the EGF-like family of protein ligands that binds to the ErbB4 receptor and activates ErbB4 receptor tyrosine phosphorylation. The EGF-like domain of NRG3 is distinct from the EGF-like domains of NRG1 and NRH2. The invention provides human and murine polypeptides (see also AAW97617) that have at beast 75% homology to the NRG3 EGF-like domain, as well as expression vectors, host cells and methods for the recombinant production of novel NRG3s. The NRG3 polypeptides and polymucleotides and can be used to enhance the survival, proliferation or differentiation of cells having

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treat damage to a nerve or damage to other NRG3-expressing or NRG3-expressing or NRG3-expressing or NRG3-expressing or NRG3-expressing or NRG3-expressing or Lie at the segonary or treat diseases which involve neural cell growth such as demyelination, or damage or loss of glial cells (e.g. multiple contains). They can be used to treat patients whose nervous system has conferenced by e.g. trauma, surgery, stroke, ischemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents.

CC metabolic disease, nutritional deficiency, malignancy, or toxic agents.

CC metabolic disease, nutritional deficiency, malignancy, or toxic agents.

CC lateral sclerosis (Lou Gehrig's disease), Bell's palsy, conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzeniers's disease, parknison's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, associated with systemic disease including post-polio syndrome, contained in the systemic disease including post-polio syndrome, contained in the systemic disease including post-polio syndrome, contained in the products of selectial muscle of smooth muscle, such as muscular dystrophy or disease caused by skeletal or smooth muscle contained immunoachesin comperises the human NRG3 EGF-like domain fused to claimed inmunoachesin comperises the human NRG3 EGF-like domain fused to
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cerebroprotective; vasotropic; antiparkinsonian; anticonvulsant;
cytostatic; nootropic; EGF; NRG-3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG66046 standard; peptide; 48 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an immunoglobulin sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 47 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CX X X X L L L L X X B X B X X B X
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The invention relates to a novel BrbB-4 ligand, neuregulin-4 (NRG-4). NRG

Disclosure; Fig 1c; 153pp; English.

Novel ErbB-4 ligand, referred as neuregulin (NRG)-4 and polynucleotide sequences encoding NRG-4, useful for upregulating or downregulating ErbB-4 receptor activity to treat Alzheimer's disease, stroke, gastric cancer.

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cc taseful for regulating an endogenous protein affecting comprising NRG-4 are recombinant methodology. Pharmaceutical compositions comprising NRG-4 are activity in vivo. They are also useful for treating or preventing a disease condition or syndrome associated with disregulation of an endogenous protein affecting arbay. Protein affecting a part of a endogenous protein affecting RPB-4 receptor activity, e.g., amyotrophic atrophy, brain trauma, stroke, ischemia, Alzheimer's disease, Parkinson's disease, epilepsy, multiple softensis, Huntington's chorea, Down's syndrome, nerve deafness, neuropathy, muscular dystrophy, extramammary paget's disease, gastric, pancreatic, prostate, breast and ovarian connection actiona, endometrial adenocarcinoma, pancreatic of calner, cervical carcinoma, endometrial adenocarcinoma, pancreatic of in the pharmaceutical composition includes a polypeptide (e.g., a soluble cligand binding domain of ErbB 4 i.e., 1984; or a monoclonal, polyclonal, humanized, single chain antibody an an immunoreactive derivative of an antibody) capable of binding the endogenous protein affecting BrbB-4 creoptor activity. Tracebble synthetic/creombinant NRG-4-tagged molecules can serve as a diagnostic tool in which cells binding the EGF-like motifs of various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Epidermal growth factor receptor; EGFR; therapy; psoriasis; carcinoma; cancer; rhabdomyosarcoma; mesothelioma; melanoma; glioblastoma; human; receptor; EGF; neuregulin 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 48;
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100.0%; Pred. No. 7.2e-21;
iive 0; Mismatches 0;
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(BIOM-) BIOMOLECULAR RES INST LTD.
(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
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או Nice EC,
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Lovrecz GO, Mckern NM,
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03-AUG-2001; 2001AU-00006828.
01-NOV-2001; 2001US-0335393P.
01-NOV-2001; 2001US-0335560P.
31-MAX-2002; 2002AU-00002731.
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2002US-0388171P.
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 48 AA;
                                                                                                                                                                                                                                                                                                                                                                       growth factors
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us-09-107-979-4.rag

of HLF activity

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The invention relates to a method of selecting or designing a compound that interacts with or inhibits the formation of active dimers of a receptor of the epidermal growth factor receptor (EGFR) family. The methods and compositions of the invention are useful for the prevention and treatment of disorders associated with signalling by a molecule of the EGFR family such as psoriasis and cancer of the pancreas, breast, brain, colon, prostate, ovary, cervix, lung, head and neck, melanoma, rhabdomyosarcoma, mesothelioma, squamous carcinomas of the skin and glioblastomas. The present sequence is epidermal growth factor (EGF) like domain of human neuregulin 3 protein. This sequence is used to illustrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated heregulin-like factor - used to develop products for the diagnosis and treatment of disorders involving regulation of cell growth,
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of active dimers of the EGF receptor family, and useful for the prevention and treatment of disorders, such as psoriasis and cancer the breast, brain or colon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human heregulin-like factor; HLF; cell growth regulator; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
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100.0%; Pred. No. 7.8e-21;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY05451 standard; protein; 157 AA
                                                                             Disclosure; Fig 2; 354pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neural system disorder; cancer
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                                                                                                                                                                                                                                                                                                         the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 47; Conservative
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                                                                                                                                                                                                                                                                                                                                            Sequence 52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New heregulin-like factor (HLF) nucleic acid or polypeptide, useful for preparing a composition for diagnosing or treating cancer.
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                               HLF; heregulin-like factor; diagnosis; cancer; gene therapy; human.
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                                                100.0%; Score 277; DB 2; Length 157; 100.0%; Pred. No. 2.1e-20; ive 0; Mismatches 0; Indels
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                                                                                                                  31 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
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Conservative 0; Mismatches
                                                                                                                                                                                                                                                                      Human heregulin-like factor (HLF) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEOU ) UNIV GEORGETOWN MEDICAL CENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 2; 48pp; English.
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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/note = EGF domain
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                                                            larity 100.0%; P
Conservative 0;
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                                                                                                                                                                                                                                              entry)
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                                                           Best Local Similarity
Matches 47; Conser
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les 47; Conserv
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N-PSDB; ADN48869.
                         Sequence 157 AA;
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Matches
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                                                                                                                                                                 RESULT 5
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AAW97621
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Gaps

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Length 52; Indels 286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCREGYQGVRCDQFL 332

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AAW97620 standard; protein; 362

RESULT 7 AAW97620

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This is the extracellular domain (ECD, aal-360 of human neuregulin related ligand NRG3 (see also AAM97618), a novel member of the epidermal growth factor (EGP)-like family of protein ligands. NRG3 binds to the ExbB4 receptor, but not to the ExbB3 or ExbB3 receptor, activates ExbB4 receptor tyrosine phosphorylation. The invention provides human and marine polypeptides (see also AAM97617) that have at least 75% homology to the NRG3 ECD, as well as expression vectors, host cells and methods for the recombinant production of novel NRG3s. The NRG3 polypeptides and can be used to enhance the survival, proliferation or differentiation of cells having the ExbB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other NRG3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat patients whose neural cell growth such a demyelination, or damage or loss of glial cells. In particular, they can be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, ischaemia, infection, metabolic disease, nutritional deficiency, dispancy, or toxic agents. NRG3 can also be used to treat motor neuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), and such as lateral sclerosis (Lou Gehrig's disease), and the such as lateral such as Albeimer's disease, particular, disease, heart motor neuron disorders such as amyotrobic lateral solerosis (Lou Gehrig's disease), and such as all and as Albeimer's disease, particular, disease, particular, disease, particular, disease, particular, disease, particular, disease, particular, disease, particular disease, particular, disease, particular disease, disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
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                                                                                                                                                                                                                                                                                                                            Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.
                                                                                                                                                                                                                    Human neuregulin related ligand NRG3 extracellular domain.
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                                                                                                                   10-MAY-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-120882/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9902681-A1
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AAW97621;
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New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.

Zhang D;

Mark MR,

Godowski PJ,

WPI; 1999-120882/10.

(GETH) GENENTECH INC.

98WO-US013411.

30-JUN-1998;

21-JAN-1999.

WO9902681-A1

Mus sp.

97US-00899437. 97US-0052019P.

24-JUL-1997;

09-JUL-1997;

Neuregulin related ligand, NRG3; mouse; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.

Mouse neuregulin related ligand NRG3 extracellular domain.

(first entry)

10-MAY-1999

AAW97620;

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This is the extracellular domain (ECD, aal-162) of murine neuregulin calated ligard NRG3 (see also AAW97617), a novel member of the epidermal carelated ligard NRG3 (see also AAW97617), a novel member of the epidermal growth factor (EGP)—like family of protein ligands. WRG3 binds to the ErbB4 receptor, but not to the ErbB3 or ErbB3 receptor, activates ErbB4 ceceptor tyrosine phosphorylation. The invention provides human and receptor tyrosine phosphorylation. The invention provides human and receptor tyrosine phosphorylation. The invention provides human and display that have at least 75% homology to the NRG3 ECD, as well as expression vectors, host cells and methods of for the recombinant production of novel NRG3s. The NRG3 polypeptides and can be used to envel or be survived. profileration or differentiation of cells having the ErbB4 receptor in vivo and in vitro. They can be used to bread diseases which involve cells. In particular, they can be used to treat diseases which involve cells (e.g. multiple sclerosis). They can be used to treat patients whose cells (e.g. multiple sclerosis). They can be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, alignancy, or toxic agents. NRG3 can also be used to treat motor neuron disorders such as amyotrophic disease, nutritional deficiency, maliphic sclerosis, fluntington, or densely as anyotrophic lateral sclerosis (Lou Gehrig's disease), adisease, epilepsy, multiple sclerosis, Huntington, or charge policy continuence, perceitations involving spinal muscular atrophy or paralysis, conditions involving spinal muscular atrophy or paralysis, conditions, involving spinal muscular atrophy or paralysis, conditions, involving spinal muscular atrophy or disease, adease, metachromatic leukodystrophy, Fabry's disease, actachromatic leukodystrophy, Fabry's disease, metachromatic leukodystrophy, Pabry's disease, actachromatic leukodystrophy, pabry's disease, such as muscular dystrophy or diseases caused by scletcal neuropathies associated w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           claim 5(a); Page 62-63; 101pp; English.
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Gaps

· 0

Indels

Length 360;

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The invention relates to human neuregulin 55, polynucleotide for coding this polypeptide and a method for producing this polypeptide by using DNA recombination technique. The invention also discloses the method for curing several diseases, such as nervous system developmental diseases, neuring several diseases, such as nervous system diseases, development disturbance, neurouss, inflammations and immunological disease by using said polypeptide. The invention also discloses an antagonist for resisting said polypeptide and its therapeutic action and also discloses the application of polynucleotide to coding this novel human neuregulin 55. The present sequence is that of human neuregulin 55.
                                                                                                                                                                                                                                                                                                 Human; neuregulin 55; nervous system; development; neuropsychopathy;
tumour; inflammation; immunological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide human neuregulin 55 and polynucleotides for encoding
                                                           0;
                                                                                                     288 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 334
                                  Length 362;
                                                                                         47
                                                             Indels
                                                                                  1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYGGVRCDQFL
                             Score 277, DB 2;
Pred. No. 4.6e-20;
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                                                          Mismatches
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                                                                                                                                                                                 ABB08776 standard; protein; 502 AA
                                                                                                                                                                                                                                                                   Human neuregulin 55 SEQ ID NO 2.
                                                        ..
                            100.0%;
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                                                                                                                                                                                                                                         16-MAY-2002 (first entry)
                                                     47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.1
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N-PSDB; ABL41244.
                                         Best Local Similarity
Sequence 362 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xie Y;
                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      CN1324826-A.
                                                                                                                                                                                                              ABB08776;
                          Query Match
                                                                                                                                                                                                                                                                                                   Human;
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                                                       Matches
                                                                                                                                                                 RESULT 8
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                                                                                                          g
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/note= "mucin-like Ser/Thr-rich region, contains sites for 0-linked glycosylation"

/note= "EGF-like domain"

.354

Domain

.360 /note= "extracellular domain, specifically claimed in claim 5(a)"

Location/Qualifiers

Homo sapiens

Domain

Region Region

'note= "hydrophobic region"

.284

101

Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; splice variant.

Human neuregulin related ligand NRG3 (splice variant).

.. 0

Gaps

10-MAY-1999 (first entry)

AAW97619;

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This is the amino acid sequence of splice variant hNGR3B2 of human ceuregulin related ligand NRG3, a novel member of the epidermal growth cartor (EGF)-like family of protein ligands that binds to the BrbB4 receptor, but not to the BrbB2 or BrbB3 receptor, and which activates treeptor, but not to the BrbB2 or BrbB3 receptor, and which activates ErbB4 receptor tyrosine phosphorylation. The sequence was deduced from the mucleotide sequence of a CDNA clone (see AAX0689) from a foetal brain library. hNGR3B2 lacks amino acids 529-552 of hNGR3B1 (see AAW97618) but retains the BGF- like domain and is expected to exhibit biological activity. The invention provides human and murine NRG3 polypeptides (see AAW97617), expression vectors, host cells and methods for the recombinant production of NRG3s. The NRG3 polypeptides and method collise having the BrbB4 receptor in vivo and in vitro. They can be used to enhance the survival, proliferation or differentiation of cells having the BrbB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other colls. In particular, they can be used to treat diseases which involve cells. In particular, they can be used to treat diseases which involve cells. Geg. multiple sclerosis). They can be used to treat patients whose colls (e.g. multiple sclerosis). They can be used to treat motor neuron collsoners such as amyotrophic lateral sclerosis flou debridy disease, and involve cells cally and sending the sending and an also be used to treat motor neuron collsoraters such as amyotrophic lateral missones in a server or disorders event as amyotrophic lateral missones in a server or disorders event as amyotrophic lateral events and methods or is a server or disorders such as amyotrophic centary and an analysis or an also be used to treat motor neuron consideration and protective centary missones and an analysis or an also be used to treat motor neuron consideration and analysis of took of also described to the consideration or damages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bell's palsy, conditions involving spinal muscular atrophy or paralys neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 78-81; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98WO-US013411.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-120882/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX06989
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0;

Gaps

; 0

47

100.0%; Score 277; DB 5; Length 502; 100.0%; Pred. No. 6.3e-20; ive 0; Mismatches 0; Indels (

92 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 138

AAW97619 standard; protein; 696 AA.

RESULT 9 AAW97619

1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL

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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention describes a polypeptide comprising an amino acid sequence encoding an epidermal growth factor (BGF)-like domain, and having the binding characteristics of neuregulin related ligand (NRG3). NRG3 polypeptide can be used to detect BrbB4 receptor in a mammalian tissue sample, and also to prevent or treat disorders associated with NRG3 such
syndrome, nerve deafness, and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including charcot-Marie-Tooth disease, Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, Fabry's disease and Dejerine-Sottas syndrome, to treat disease of skeletal muscle of smooth muscle, such as muscular dystrophy or diseases caused by skeletal or smooth ensele wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A new neuregulin related ligand designated NRG3 has an epidermal growth factor-like domain and binds to ErbB4 receptor, and is useful to prevent or treat NRG3 associated disorders, particularly nerve damage.
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                              Score 277; DB 2; Length 696; Pred. No. 8.4e-20;
                                                                                                                                                                                                                                                                                                                         47
                                                                                                                                                                                                                                                                                                                       1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human neuregulin related ligand NRG3B2.
                                                                                                                                                                                                                                100.0%; Scor.
100.0%; Pred. No. c.
0, Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0053641P.
98US-00107979.
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Best Local Similarity 100.7
Matches 47; Conservative
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                                                                                                                                                                                                                    Sequence 696 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-JUL-1997;
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                                                                                                                                                                                   screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG32080;
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                 888888888888%
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as: amyotrophic lateral sclerosis (low Gehrig's disease), Bell's palsy and various conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntingdon's chorea, Down's syndrome, nerve deafness, Meniere's disease, neuropathy such as distal sensorimotor neuropathy or autonomic neuropathy, hereditary neuropathies such as Charcot-Marie-Tooth disease, Reisease, Abetalipoproteinaemia, Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Rabry's disease and Dejerine-Scottas syndrome. This is the amino acid sequence of the novel human neuregulin related ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105..286,
/note= "mucin-like Ser/Thr-rich region, contains sites
for O-linked glycosylation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "extracellular domain, specifically claimed in claim 5(a)"
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuregulin related ligand; NRG3; mouse; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.
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0
                                                                                                                                                                                                                                                                          286 HFKPCRDKDLAYCLNDGBCFVIETLTGSHKHCRCKBGYQGVRCDQFL 332
                                                                                                                                                                                                    Length 696;
                                                                                                                                                                                                                                                        47
                                                                                                                                                                                                                                                        1 HEKRCKDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
                                                                                                                                                                                                                                Indels
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8.4e-20;
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/note= "transmembrane domain"
                                                                                                                                                                                                    100.0%; Score 277; DB 100.0%; Pred. No. 8.4e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "hydrophobic region"
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "EGF-like domain"
363. .385
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse neuregulin related ligand NRG3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'n
                                                                                                                                                                                                                                                                                                                                                         AAW97617 standard; protein; 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0052019P.
97US-00899437.
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Godowski PJ, Mark MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-120882/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAX06987.
                                                                                                                                                                               Sequence 696 AA;
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                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                 RESULT 11
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us-09-107-979-4.rag

This is the amino acid sequence of murine neuregulin related ligand NRG3, a novel member of the epidermal growth factor (EGF)-like family of protein ligands that binds to the ErbB4 receptor, but not to the ErbB2 or ErbB3 receptor, and which activates ErbB4 receptor, but not to the ErbB2 or phosphorylation. The sequence was deduced from the nuclectide sequences of CTMA clones (see AXX06987) from a mouse brain library. The EGF-like commain of NRG3 is distinct from those of NRG1 or NRG3, and NRG3 displays receptor binding characteristics that are distinct from those of other neuregulins. The invention provides human and murine NRG3 polypeptides (see also AAW97618), expression vectors, host cells and methods for the recombinant production of NRG3. The NRG3 polypeptides and can be used to enhance the survival, proliferation of cells having the ErbB4 receptor in vivo and in viro. They can be used to prevent or treat damage to other (CT Prey can be used to prevent or treat damage to other (CT Prey can be used to prevent or treat damage to a nerve or damage to other (CT Prey can be used to prevent or treat damage to seed to reat patients whose cells (e.g. multiple sclerosis). They can be used to treat patients whose cells (e.g. multiple sclerosis). They can be used to treat motor neuron ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents. NRG3 can also be used to treat motor neuron Eschaemia, infection, metabolic disease, nutritional deficiency, disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), EBIS palsy, conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzenewer's disease, Parkinson's chaese, epilensy. Multiple sclerosis, Huntinoron's chorea. Damage of disease, Damage, CT di disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's syndrome, nerve deafness, and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including Charcot-Marie-Tooth disease, syndrome, hereditary neuropathies including charton frames, Krabbe's Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, Fabry's disease and Dejerine-Sottas syndrome, to treat disease of skeletal muscle of smooth muscle, such as muscular dystrophy or diseases caused by skeletal or smooth such as muscular dystrophy or diseases caused by skeletal or smooth such as muscular dystrophy or diseases. muscle wasting. The products can also be used for detection, diaged the production of transgenic or knockout animals or for drug Claim 5(b); Page 59-62; 101pp; English. screening

Sequence 713 AA;

Gaps ·. 100.0%; Score 277; DB 2; Length 713; 100.0%; Pred. No. 8.6e-20; Indels Query Match
Best Local Similarity 100.0%; Pred. No. b.o.
Matches 47; Conservative 0; Mismatches

0

47

1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 288

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RESULT 12 ABG32061

ABG32061 standard; protein; 713 AA

ABG32061;

05-NOV-2002 (first entry)

Mouse novel neuregulin related ligand NRG3.

Neuregulin related ligand; NRG3; neuroprotective; cell therapy; ErbB4 receptor detection; amyotrophic lateral sclerosis; paralysis; lou Gehrig's disease; spinal muscular atrophy; multiple sclerosis; perplepsy; huntingon's crorea; Down's syndrome; nerve deafness; Meniers's disease; neuropathy; distal sensorimetor neuropathy; autonomic neuropathy; hereditary neuropathy; Charcor neuropathy; autonomic neuropathy; hereditary neuropathy; Charcor neuropathy; Refsum's disease; Aberalipoproteinaemia; Tangier disease; Krabbe's disease; Metanhromatic leukodystrophy; Rabry's disease; Dejerine-Scottas syndrome; mouse.

Mus sp

Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.

Human neuregulin related ligand NRG3.

(first entry)

10-MAY-1999

AAW97618;

AAW97618 standard; protein; 720 AA.

AAW97618

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The invention describes a polypeptide comprising an amino acid sequence encoding an epidermal growth factor (EGF)-like domain, and having the encoding an epidermal growth factor (EGF)-like domain, and having the binding characteristics of neuregulin related ligand (NRG3). NRG3 polypeptide can be used to detect ExbB4 receptor in a mammalian tissue sample, and also to prevent or treat disorders associated with NRG3 such as amyotrophic lateral sclerosis (lou Gehrig's disease). Bell's palsy and various conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntingdon's chorea, Down's syndrome, nerve deafness, Meniere's disease, neuropathy such as distal sensorimotor neuropathy or autonomic neuropathy, hereditary neuropathies such as Charcot-Marie-Tooch disease, Refsum's disease, Metachromatic leukodystrophy, Pabry's disease and Dejezine-Scottas syndrome. This is the main acid sequence of the novel mouse neuregulin related ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    A new neuregulin related ligand designated NRG3 has an epidermal growth factor-like domain and binds to ErbB4 receptor, and is useful to prevent or treat NRG3 associated disorders, particularly nerve damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                      /note= "ExtracelTular epidermal growth factor-like domain. Specifically claimed in claim 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 334
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    .362
    /label= Extracellular domain
    /note= "Specifically Claimed in claim 5"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                    288. .334
/label= EGF-like_domain
 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Fig 4A-B; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                    Zhang D;
                                                                                                                                                                                                                                      26-MAR-2001; 2001US-00817647.
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98US-00107979.
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Best Local Similarity 100.0
                                                                                                                                                                                                                                                                                                                                                                  Godowski PJ, Mark MR,
                                                                                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-617760/66.
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                                                                                                                                                              US2002082229-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 713 AA;
                                                                                                                                                                                                                                                                      24-JUL-1997;
                                                                                                                                                                                                                                                                                           30-JUN-1998;
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                 Domain
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screening

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This is the amino acid sequence of human neuregulin related ligand NRG3, can novel member of the epidermal growth factor (EGF)-like family of protein ligands that binds to the Erb84 receptor, but not to the Erb82 or Erb81 receptor, but not to the Erb82 or Erb81 receptor, but not to the Erb82 or Erb83 receptor, but not to the Erb82 or Erb83 receptor, and which activates Erb84 receptor tyrosine prosphorylation. The sequence was deduced from the nucleotide sequence of a cDNA clone (see AAXC088) from a foetal brain library. The EGF-like a cDNA clone (see AAXC088) from a foetal brain library. The EGF-like comain of NRG3 is distinct from those of to the receptor binding characteristics that are distinct from those of characteristics that are distinct from those of characteristics of the sequence of provides human and murine NRG3 is provided in neuregulins. An alternatively spliced form of human in the NRG3 by peptides (see also AMW97617), expression vectors, host cells and methods for the calls on the used to enhance the survival proliferation of differentiation of cells having the Erb84 receptor in vivo and in vitro. Cifferentiation of cells having the Erb84 receptor in vivo and in vitro. MRG3-expressing or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat diseases which involve cells (e.g. multiple sclerosis). They can be used to treat patients whose cells (e.g. multiple sclerosis). They can be used to treat patients whose cells (e.g. multiple sclerosis). They can be used to treat patients whose instruction, metabolic disease, patients of sease, patients whose malgamery, or toxic agents. NRG3 can also be used to treat patients and sangeronial miscilar atrophy or paralysis, cellsoreders under a supercort. Marte-Toth disease, syndrome, nerve deafness, and Meniere's disease. They can be used to treat meuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including charge to small or syndrome. The products of treat meuropath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
                                                                                                                                                                  /note= "mucin-like Ser/Thr-rich region, contains sites for O-linked glycosylation"
                                                              /note= "extracellular domain, specifically claimed in Claim 5(a)"
                                                                                                                                                                                                                                                                   /note= "transmembrane domain"
                                                                                                                               "hydrophobic region"
                                                                                                                                                                                                                      /note= "EGF-like domain"
356. .394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 5(b); Page 66-69; 101pp; English.
                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhang D;
                                                                                                                                                                                                                                                                                                                                                                                      98WO-US013411.
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97US-00899437.
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                                                        .360
                                                                                                                                   'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-120882/10.
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                                                                                                                                                                                                                                                                                                             WO9902681-A1.
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  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence is the human heregulin-like factor (HLF) of the invention. The HLF is involved in the regulation of cell growth. Detection of different levels of expression of the HLF gene can be used for the diagnosis of disorders, e.g. in the neural system. In particular, detection of different levels of HLF gene expression in cells or body fluid of an individual can be used for diagnosing cancer. The products can also be used in the treatment of disorders involving abnormal levels of HLF activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated heregulin-like factor - used to develop products for the diagnosis and treatment of disorders involving regulation of cell growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                         Gaps
                                                                                                                                                                                                                                                                                                          factor; HLF; cell growth regulator; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                         0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 720;
                                                                                                                    286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKBGYQGVRCDQFL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                             Length 720;
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                                                                         Indels
                                                                                                  1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
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100.0%; Pred. No. 8.7e-20;
iive 0; Mismatches 0;
                                     100.0%; Score 277; DB 4;
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                                                               Pred. No. 8.7
Mismatches
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                                                                                                                                                                                                                                                                                 Human heregulin-like factor sequence.
                                                                                                                                                                                                    AAY05452 standard; protein; 720 AA
                                                   100.08; F1
                                                                                                                                                                                                                                                                                                                              neural system disorder; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     King CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US012403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0049942P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                            (first entry)
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Matches 47; Conservative
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEOU ) UNIV GEORGETOWN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      particularly cancers
                                                                                                                                                                                                                                                                                                                Human heregulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Young P, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-095327/08
                                                   Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 720 AA;
                         Sequence 720 AA;
                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                  AAY05452;
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                                                                                                                                                                             RESULT 14
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S X S
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ABG32065 standard; protein; 720 AA.

ABG32065

(first entry)

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Human novel neuregulin related ligand NRG3B1.
                                        05-NOV-2002
ABG32065;
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Neuregulin related ligand; NRG3; neuroprotective; cell therapy; epidermal growth factor—like domain; EGF-like domain; Bell's pall's pall's brider receptor detection; amyotrophic lateral sclerosis; paralysis; lou Gehrig's disease; spinal muscular atrophy; multiple sclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; Huntingdon's chorea; Down's syndrome; nerve deafness; Meniere's disease; neuropathy; distal sensorimotor neuropathy; autonomic neuropathy; hereditary neuropathy; Charoct-Marie-Tooth disease; Refsum's disease; Abetalipoproteinaemia; Tangier disease; Metachromatic leukodystrophy; Fabry's disease; Dejerine-Scottas syndrome; human; gene; ss; NRG3B1.
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Homo sapiens.

/label= EGF-like domain /note= "Extracellular epidermal growth factor-like Location/Qualifiers Domain Domain

US2002082229-A1.

domain"

27-JUN-2002

26-MAR-2001; 2001US-00817647.

97US-0053641P. 98US-00107979. 24-JUL-1997; 30-JUN-1998;

(GETH) GENENTECH INC

Zhang D; Godowski PJ, Mark MR,

WPI; 2002-617760/66. N-PSDB; ABK90731 A new neuregulin related ligand designated NRG3 has an epidermal growth factor-like domain and binds to ErbB4 receptor, and is useful to prevent or treat NRG3 associated disorders, particularly nerve damage.

Example 1; Fig 4A-B; 60pp; English

The invention describes a polypeptide comprising an amino acid sequence encoding an epidermal growth factor (EGF)-like domain, and having the binding characteristics of neuregalian related ligand (NRG3) NRG3 polypeptide can be used to detect EnbB4 receptor in a mammalian tissue sample, and also to prevent or treat disorders associated with NRG3 such as: amyotrophic lateral sclerosis (lou Gehrig's disease), Bell's palsy and various conditions involving spinal muscular atrophy or paralysis, and various conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntingdon's chorea, Down's syndrome, nerve deafness, Meniere's disease, neuropathy such as distall sensorimotor neuropathy or autonomic neuropathy, hereditary neuropathies such as Charcot-Marie-Tooth disease, Refsum's disease, Metachromatic leukodystrophy, Fabry's disease and Dejerine-Scottas syndrome. This is the amino acid sequence of the novel human neuregulin related ligand

Sequence 720 AA;

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                                                                     0; Gaps
Query Match 100.0%; Score 277; DB 5; Length 720; Best Local Similarity 100.0%; Pred. No. 8.7e-20; Matches 47; Conservative 0; Mismatches 0; Indels (
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1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 47	SECFVIETLTGS
	28
δ	qa

2, 2004, 13:24:19 Search completed: November Job time

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                 Copyright
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- protein search, using sw model OM protein

November 2, 2004, 13:28:26; Search time 156 Seconds (without alignments) 108.079 Million cell updates/sec Run on:

US-09-107-979-4

1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL 47 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

2002273 seqs, 358729299 residues Searched:

0

Word size

2002273 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Listing first 45

A_Geneseq_23Sep04:* 1: genesemnaeaaa geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2002s:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqp2004s:*

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Result No.	Score	Query	Length	DB	ID	Description
ત	47	100.0	47	i N	AAW97622	April CONTRACT
7	47	100.0	48	'n	AAG66046	Hamai
3	47	100.0	5.2	1 4	AAE36807	Mouse
4	47	100.0	157	0	AAV05451	Human
Ŋ	47	100.0	157	ια	ADM48870	нишап
9	47	100.0	360	0	AAW97621	
7	47	100.0	362	N	AAW97620	Mondo
ω	47	100.0	502	Ľ	ABB08776	House
σ	47	100.0	969	(AAW97619	Homor
10	47	100.0	969	ו נר	ARC3 2080	Human
11		100.0	713	٠ (712022000 71370344	Nove
12		100	1 1	1 4	1700000	
1 .	• •	0.00	170	n	ABG32061	Abg32061 Mouse nov
7 -	7,	100.0	720	~	AAW97618	Aaw97618 Human neu
4 1	4.7	100.0	720	N	AAY05452	
15	47	100.0	720	'n	ABG32065	Human
16	47	100.0	720	ω	ADN48890	Human
17	α	17.0	80	N	AAW97623	
18	80	17.0	6 0	Ŋ	ABG32078	
19	7	14.9	87	4	AA006698	
20	7	4	156	m	AAG37655	
21	7	14.9	168	~	AAC34461	
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47	7	4	207	m	AAG37654	Arabid
52	7	14.9	219	r	AAG34460	

Aag37653 Arabidops Aag34459 Arabidops	Aag05216 Arabidops Aag39240 Arabidops	Abm73948 DNA clone Aad39239 Arabidons				Abg93885 Wheat ami	-									
AAG37653 AAG34459	AAGU5216 AAG39240	ABM73948 AAG39239	AAG36778	AAG05215	ABM73802	ABG93885	ADF66727	ABG93884	ADF66725	AAG05214	AAG36777	AAG39238	ABO01340	ADN96052	AAG36776	ADM74187
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237	349 949	349	357	357	377	401	401	407	407	408	408	408	450	450	452	471
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27	29	30 31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

Human neuregulin related ligand NRG3 EGF-like domain. AA. AAW97622 standard; protein; 47 (first entry) 10-MAY-1999 AAW97622; AAW97622

Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; epidermal growth factor; EGF; immunoadhesin.

Homo sapiens.

WO9902681-A1.

21-JAN-1999.

98WO-US013411. 30-JUN-1998; 97US-0052019P. 97US-00899437. 09-JUL-1997; 24-JUL-1997;

(GETH) GENENTECH INC.

ä Zhang Mark MR, Godowski PJ,

WPI; 1999-120882/10.

New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzhelmer's disease or Down's syndrome.

Claim 30; Page 64; 101pp; English.

This is the epidermal growth factor (EGF)-like domain of human neuregulin related ligand NRG3 (see also AAW97618), a novel member of the EGF-like family of protein ligands that binds to the ErbB4 receptor and activates ErbB4 receptor tyrosine phosphorylation. The EGF-like domain of NRG3 is distinct from the EGF-like domains of NRG1 and NRH2. The invention provides human and murine polypeptides (see also AAW97617) that have at least 75% homology to the NRG3 EGF-like domain, as well as expression vectors, host cells and methods for the recombinant production of novel NRG3s. The NRG3 polypeptides and polynucleotides and can be used to enhance the survival, proliferation or differentiation of cells having

and can be expressed by standard

to mammalian ErbB-4 receptor

- 4 binds to mammalian krbb-4 receptor aun can be explessed by clearance to recombinant methodology. Pharmaceutical compositions comprising NRG-4 are recombinant methodology. Pharmaceutical compositions comprising NRG-4 are useful for regulating an endogenous protein affecting ErbB-4 receptor activity in vivo. They are also useful for treating or preventing a activity in vivo. They are also useful for treating or preventing a cativity in vivo. They are also useful for treating or preventing a cativity in vivo. They are also useful for treating or preventing a cativity in vivo. They are also useful for treating or preventing a cativity, e.g., amyotrophic endogenous protein affecting BrbB-4 receptor activity, e.g., amyotrophic catrophy, brain trauma, stroke, ischemia, Alzheimer's disease, Parkinson's disease, epilepsy, multiple solerosis, Huntington's chorea, Down's syndrome, nerve deafness, neuropathy, muscular dystrophy, extramammary caper, s disease, gastric, pancreatic, prostate, breast and ovarian cancer, cervical carcinoma, endometrial adenocarcinoma, pancreatic D cancer, cervical carcinoma, endometrial adenocarcinoma, pancreatic D cancer, cervical carcinoma, endometrial adenocarcinoma, pancreatic C calles-somatostatinoma and Zollinger-Ellison syndrome. The agent comprised in the pharmaceutical composition includes a polypeptide (e.g., a soluble conting domain of ErbB-4 i.e., IGB4; or a monoclonal, polyclonal, humanized, single chain antibody or an immunoreactive derivative of an erceptor activity. Traceable synthetic/recombinant NRG-4 canged molecules can serve as a diagnostic tool in which cells binding NRG-4 can be conserved.

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the ErbB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other NRG3-expressing or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat diseases which involve neural cell growth such as demyelination, or damage or loss of glial cells (e.g. multiple contains). They can be used to treat patients whose nervous system has celerosis. They can be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, ischaemia, infection, metabolic disease, nutritional deficiency, malignancy, or toxic agents. They can also be used to treat motor neuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alabeimer's disease, Parkinson's disease, epilepsy, and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including charcot-Marie-Tooth disease, actions associated with systemic disease including charcot-Marie-Tooth disease, contains as associated with systemic disease including charcot-Marie-Tooth disease, such as section and the systemic disease classes and mobilerine-Sottas contains the products on sisease caused by skeletal or smooth muscle, such as wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug screening. A criamed inmunoadhesin comparises the human NRG3 EGF-like domain fused to
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cerebroprotective; vasotropic; antiparkinsonian; anticonvulsant;
cytostatic; nootropic; EGF; NRG-3.
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Matches
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Sequence 48 AA; growth factors

Query Match

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cancer; rhabdomyosarcoma; mesothelioma; melanoma; glioblastoma; human;
receptor; EGF; neuregulin 3.
                          Gaps
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                                                1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
100.0%; Score 47; DB 5; Length 48; 100.0%; Pred. No. 3.6e-41;
                        0; Indels
                                                                2 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKBGYQGVRCDQFL
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e EC, Ward CW;
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cern NM, Nice EC,
                            0; Mismatches
                                                                                                                                                                                                                 Human neuregulin 3 EGF-like domain.
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Lovrecz GO, Mckern NM,
                                                                                                                                         AAE36807 standard; protein; 52
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03-AUG-2001; 2001AU-00006828.
01-NOV-2001; 2001US-0335393P.
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2002AU-00002731.
2002US-0388171P.
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                                                                                                                                                                                           (first entry)
               Local Similarity 100.
nes 47; Conservative
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31-MAY-2002;
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                                                                                                                                                                   AAE36807;
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                               Matches
                                                                                                                    RESULT 3
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Novel ErbB-4 ligand, referred as neuregulin (NRG)-4 and polynucleotide sequences encoding NRG-4, useful for upregulating or downregulating ErbB-4 receptor activity to treat Alzheimer's disease, stroke, gastric cancer.

Yarden Y;

Harari D,

WPI; 2002-041398/05.

The invention relates to a novel ErbB-4 ligand, neuregulin-4 (NRG-4). NRG

Disclosure; Fig 1c; 153pp; English

.. 0

Gaps

. 0

Length 157;

100.0%; Score 47; DB 2; Length 15 100.0%; Pred. No. 1e-40; ive 0; Mismatches 0; Indels

47; Conservative

Matches

à

Local Similarity

Query Match

Sequence 157 AA; of HLF activity

SXS

1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL

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AAY05451;
                         Young P,
         Matches
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The invention relates to a method of selecting or designing a compound that interacts with or inhibits the formation of active dimers of a receptor of the epidermal growth factor receptor (EGFR) family. The methods and compositions of the invention are useful for the prevention and treatment of disorders associated with signalling by a molecule of the EGFR family such as psoriamis and cancer of the pancreas, breast, brain, colon, prostate, ovary, cervix, lung, head and neck, melanoma, rhabdomyosarcoma, mesothelioma, squamous carcinomas of the skin and glioblastomas. The present sequence is epidermal growth factor (EGF) like domain of human neuregulin 3 protein. This sequence is used to illustrate
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of active dimers of the EGF receptor family, and useful for the prevention and treatment of disorders, such as psoriasis and cancer of the breast, brain or colon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY05451 standard; protein; 157 AA
                                                                                                                                  Disclosure; Fig 2; 354pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the method of the invention
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     New heregulin-like factor (HLF) nucleic acid or polypeptide, useful for preparing a composition for diagnosing or treating cancer.
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                                                                                                                                                               HLF; heregulin-like factor; diagnosis; cancer; gene therapy; human.
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31 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 47; DB 8; Length 157; 100.0%; Pred. No. 1e-40; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
                                                                                                                                          (HLF) protein.
                                                                                                                                                                                                                                                                                                                                                                                                Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                        CENT.
                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 2; 48pp; English
                                                                    ADN48870 standard; protein; 157 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW97621 standard; protein; 360 AA.
                                                                                                                                                                                                                                                                                                                                                                    (GEOU ) UNIV GEORGETOWN MEDICAL
                                                                                                                                                                                                                                                                                                                                                                                               Hijazi M,
                                                                                                                                                                                                                                                                                                                                   97US-0049492P.
                                                                                                                                                                                                                                                                                                            98US-00097681.
                                                                                                                                        Human heregulin-like factor
                                                                                                                                                                                                                            26. .93
/note = EGF
                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                             King CR,
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N-PSDB; ADN48869.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 157 AA;
                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                           16-JUN-1998;
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                                                                                                                  15-JUL-2004
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                                            RESULT 5
ADN48870
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AAW97621
ID AAW9
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This is the extracellular domain (ECD, aal-360 of human neuregulin related ligand NRG3 (see also AAW97618), a novel member of the epidermal calated ligand NRG3 (see also AAW97618), a novel member of the epidermal growth factor (EGF)-like family of protein ligands. NRG3 binds to the ETDB4 receptor, but not to the ETDB4 receptor, activates ETDB4 receptor tyrosine phosphorylation. The invention provides human and receptor tyrosine phosphorylation. The invention provides human and the NRG3 ECD, as well as expression vectors, host cells and methods to the NRG3 ECD, as well as expression vectors, host cells and methods of cort he recombinant production of novel NRG3s. The NRG3 polypeptides and can be used to enhance the survival, proliferation or differentiation of cells having the ETDB4 receptor in vivo and in vitro. They can be used to treat diseases which involve cells. In particular, they can be used to treat diseases which involve neural cell growth such as demyelination, or damage to a lost of gilal cells (e.g. multiple sclerosis). They can be used to treat patients whose cells (e.g. multiple sclerosis). They can be used to treat motor neuron system has been damaged by e.g. trauma, surgery, stroke, alignment, or toxic agents. NRG3 can also be used to treat motor neuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), a disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's confiscome, nervo designess, metaral sclerosis (Lou Gehrig's disease, Down's confiscome, nervo designess und Meniere's disease, and Delerine syndrome, nervo designess, mathington's chorea, prophy parally sclerosis, Huntington's chorea, Down's confiscase, metachromatic leukodystrophy, Pabry's disease, and Delerine sponderiement, and Meniere signisease and Delerine successive contras syndrome, to treat disease of skeletal muscle of smooth muscle wasting. The products can also be used for detection, diagnosis, contas syndrome, percentageneral sclerosis and sease caused of smooth of transgenic or knockout animal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
                                                                                                                                                                                                                                           Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.
                                                                                                                                                            Human neuregulin related ligand NRG3 extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5(a); Page 69-70; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang D;
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                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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AAW97621;
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Query Match 100.0%; Score 47; DB 2; Length 360; Best Local Similarity 100.0%; Pred. No. 2.1e-40; Matches 47; Conservative 0; Mismatches 0; Indels
Sequence 360 AA;
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This is the extracellular domain (ECD, aal-362) of murine neuregulin crelated ligand NRG3 (see also AAM97617), a novel member of the epidermal correlated ligand NRG3 (see also AAM97617), a novel member of the epidermal correction (ECD) and the correction of the creeptor but not to the ErbB2 or ErbB3 receptor, activates ErbB4 receptor tyrosine phosphorylation. The invention provides human and receptor tyrosine phosphorylation. The invention provides human and conceptor tyrosine phosphorylation. The invention provides human and conceptor tyrosine phosphorylation. The invention provides human and methods to the recombinant production of novel NRG3 but to say from the condition of cells as expression vectors, host cells and methods of inferentiation of cells having the ErbB4 receptor in vivo and in vitro. differentiation of cells having the ErbB4 receptor in vivo and in vitro. In NRG3-expressing or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat diseases which involve cells. In particular, they can be used to treat parients whose cells. In particular, and amaged by e.g. trauma, surgery, stroke, neural cell growth such as demyelination, or damage to treat parients whose cells in fection, metabolic disease, nutritional defliciency, ischaemia, infection, metabolic disease, nutritional defliciency.

Collamma, infection, metabolic disease, nutritional defliciency, stroke, schaemia, infection, metabolic disease, nutritional collamma and the collamma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
                                                                                                                                                                                                                                                                                                   Neuregulin related ligand; NRG3; mouse; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.
286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332
                                                                                                                                                                                                                                                              Mouse neuregulin related ligand NRG3 extracellular domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5(a); Page 62-63; 101pp; English.
                                                                                                                                       AAW97620 standard; protein; 362 AA
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97US-00899437.
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                                                                                                                                                                                                                              (first entry)
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The invention relates to human neuregulin 55, polymucleotide for coding relais polypeptide and a method for producing this polypeptide by using DNA recombination technique. The invention also discloses the method for curing several diseases, such as nervous system developmental diseases, neuropsychopathy, other nervous system diseases, development disturbance, neuropsychopathy, other nervous system disease, development disturbance, polypeptide. The invention and immunological disease by using said polypeptide and its therapeutic action and also discloses the application of polymucleotide to coding this novel human neuregulin 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; neuregulin 55; nervous system; development; neuropsychopathy;
tumour; inflammation; immunological disease.
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                                                                                                                                                                                                                                                  288 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 334
                                                                                                                                                                                                                      47
                                                                              Length 362;
                                                                                                                                           0; Indels
                                                                                                                                                                                                1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
                                                                       Score 47; DB 2; Pred. No. 2.1e-40;
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                                                                                                                                       Mismatches
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100.0%; Cost Similarity 100.0%; Pred. No. 2.8
Matches 47; Conservative 0; Mismatches
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                                              100.0%; Scor
100.0%; Pre
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                                                                                                                                47; Conservative
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N-PSDB; ABL41244.
                                                                                                   Local Similarity
Sequence 362 AA;
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                                                                Query Match
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                                                                                                                                    Matches
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. 0 Gaps ; 0 1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47 100.0%; Score 47; DB 5; Length 502; 100.0%; Pred. No. 2.8e-40; 0; Indels

AAW97619 standard; protein; 696 AA.

AAW97619 ID AAW9 XX RESULT 9

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This is the amino acid sequence of splice variant hNGR3B2 of human neuregulin related ligand NRG3, a novel member of the epidermal growth activates that but new to the ErbB3 or ErbB3 receptor, and which activates be tractor (EGF)-like family of protein ligands that binds to the ErbB4 receptor, but not to the ErbB2 or ErbB3 receptor, and which activates ErbB4 receptor tyrosine phosphorylation. The sequence was deduced from brain library. hNGR3B2 lacks amino acids 529-552 of hNGR3B1 (see ErbB4 receptor tyrosine phosphorylation. The sequence was deduced from brain library. hNGR3B2 lacks amino acids 529-552 of hNGR3B1 (see ErbB4 protein and is expected to exhibit complyagetides (see AAW97617), expression vectors, host calls and methods for the recombinant production of MRG3s. The NRG3 polypaptides and methods for the recombinant production of MRG3s. The NRG3 polypaptides and methods complyagetides and can be used to enhance the survival, proliferation or differentiation of cells having the ErbB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other CC MRG3-expressing or NRG3-responsive cells, e.g. brain, heart, or kidney cells. In particular, they can be used to treat diseases which involve cells. In particular, they can be used to treat patients whose cells (e.g. multiple sclerosis). They can be used to treat motor neuron disorders such as amyotrophic lateral sclerosis flow dehrig's disease), conditions involving spinal muscular atrophy or paralysis, conditions involving spinal muscular atrophy or paralysis, conneurodegenerative disorders such as Salzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntington's chorea, Down's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
                                                                                                                                                                                                                                                                                                                                                                 /note= "mucin-like Ser/Thr-rich region, contains sites for O-linked glycosylation"

    .360
/note= "extracellular domain, specifically claimed in
Claim 5(a)"

                                                                                                             Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor;
                                                                                                                                   signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis; splice variant.
                                                                         Human neuregulin related ligand NRG3 (splice variant)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "transmembrane domain"
                                                                                                                                                                                                                                                                                                                        /note= "hydrophobic region"
                                                                                                                                                                                                                                                                                                                                                                                                                         note= "EGF-like domain"
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                                                                                                                                                                                                                                Location/Qualifiers
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97US-00899437.
                                     (first entry)
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                                   10-MAY-1999
                                                                                                                                                                                            Homo sapiens
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 AAW97619
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syndrome, nerve deafness, and Meniere's disease. They can also be used to treat neuropathies associated with systemic disease including post-polio syndrome, hereditary neuropathies including charcot-Marie-Tooth disease, Refsum's disease, abetalipoproteinemia, Tangier disease, Krabbe's disease, metachromatic leukodystrophy, Pabry's disease and Dejerine-Sottas syndrome, to treat disease of skeletal muscle of smooth muscle, such as muscular dystrophy or diseases caused by skeletal or smooth muscle wasting. The products can also be used for detection, diagnosis, for the production of transgenic or knockout animals or for drug
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a polypeptide comprising an amino acid sequence encoding an epidermal growth factor (EGF)-11ke domain, and having the binding characteristics of neurequlin related ligand (NRG3). NRG3 polypeptide can be used to detect Brb84 receptor in a mammalian tissue sample, and also to prevent or treat disorders associated with NRG3 such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful to prevent damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           growth
                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                     1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                 Length 696;
                                                                                                                                                                                                                                                                                  0; Indels
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; Pred. No. 3.7e-40;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          syndrome; human; NRGB2
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nes 47; Conservative
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                                                                                                                                                                                                                  Sequence 696 AA;
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Matches
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as: amyotrophic lateral sclerosis (lou Gehrig's disease), Bell's palsy and various conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntingdon's chorea, Down's syndrome, nerve deafness, Meniere's disease, neuropathy such as distal sensorimetor neuropathy or autonomic neuropathy, hereditary neuropathies such as Charcot-Marie-Tooth disease, Refsum's disease, Metachromatic leukodystrophy, Pabry's disease and Dejerine-Scottas syndrome. This is leukodystrophy, Pabry's disease and Dejerine-Scottas syndrome. This is the amino acid sequence of the novel human neuregulin related ligand NRG3B2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
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287. .334

    362
/note= "extracellular domain, specifically claimed in
Claim 5(a)"
    91

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signal transduction; nervous system disorder; neurodegeneration;
neuropathy; therapy; diagnosis.
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100.0%; Pred. No. 3.7e-40;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "hydrophobic region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "EGF-like domain"
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97US-00899437.
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Best Local Similarity
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                                                                                                                                                                                      Sequence 696 AA;
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This is the manner oath dequence of murine neuregulin related ligand NRG3, a novel member of the epidermal growth factor (EGT)-like family of protein ligands that binds to the grbb4 factor (EGT)-like family of ETDB3 receptor, but not to the ETDB2 or C of ETDB3 close (ETDB3 etDB4 receptor through the ETDB3 or ETDB4 receptor the mucleotide sequences of C on ETDB4 close (See AAXO6997) from a mouse brain library. The EGF-like c creeptor binding characteristics that are distinct from those of other c neuregulins. The invention provides human and murine NRG3 polypeptides crecombinant production of NRG3s. The NRG3 polypeptides and can be used to enhance the survival, proliferation of polynucleotides and can be used to enhance the survival, proliferation of differentiation of cells having the ETDB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other cells. In particular, they can be used to treat patients whose nerval cells growth such as demyelination, or damage or loss of glial cells. In particular, they can be used to treat patients whose nervous system has been damaged by e.g. trauma, surgery, stroke, malignancy, or toxic agents NG3-reads, murritional deficiency, multiple sclerosis, function, metabolic disease, murritional deficiency, multiple sclerosis, Huntington's chorea, Down's disease, prolepsy, multiple sclerosis, Huntington's chorea, Down's disease, pepilepsy, multiple sclerosis, Huntington's chorea, Down's disease, pepilepsy, multiple sclerosis, Huntington's chorea, Down's disease, pepilepsy, multiple sclerosis, Huntington's chorea, Down's settle spale associated with systemic disease including post-polic syndrome, hereditary neuropathies including charcot-Marie-Tooth disease, abetalioporteinemia, Tangier disease and Dejering for the production of transgenic or knockout animals or for druggeness. This is the amino acid sequence of murine neuregulin related ligand NRG3, Claim 5(b); Page 59-62; 101pp; English.

Sequence 713 AA;

Gaps ·. Query Match 100.0%; Score 47; DB 2; Length 713; Best Local Similarity 100.0%; Pred. No. 3.8e-40; Matches 47; Conservative 0; Mismatches 0; Indels

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ABG32061 standard; protein; 713 AA. ABG32061; RESULT 12 ABG32061

(first entry) 05-NOV-2002

Neuregulin related ligand; NRG3; neuroprotective; cell therapy; ErbB4 receptor detection; amyotrophic lateral sclerosis; paralysis; lou Gehrig's disease; spinal muscular atrophy; multiple sclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; henringdon's chorea; Down's syndrome; nerve deafness; meniconnic neuropathy; hereditary neuropathy; charcor-meuropathy; autonomic neuropathy; hereditary neuropathy; Charcor-merie-Tooth disease; Krabbe's disease; Metalipoproteinaemia; Tangier disease; Abetalipoproteinaemia; Tangier disease; Actabe's disease; Metalipoproteinaemia; Tangier disease; Mouse novel neuregulin related ligand NRG3.

Dejerine-Scottas syndrome; mouse.

Mus sp.

The invention describes a polypeptide comprising an amino acid sequence encoding an epidermal growth factor (EGF)-like domain, and having the binding characteristics of neuregulin related ligand (NRG3). NRG3 polypeptide can be used to detect ErbB4 receptor in a mammalian tissue sample, and also to prevent or treat disorders associated with NRG3 such as: amycorrophic lateral sclerosis (lou Gehrig's disease), Bell's palsy and various conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's syndrome, nerve deafness, Meniere's disease, neuropathy such as distal sensorimotor neuropathy or autonomic neuropathy, hereditary neuropathies such as Charcot Marie-Tooth disease, eneuropathy eneuropathies such as Charcot Marie-Tooth disease, eneuropathies A new neuregulin related ligand designated NRG3 has an epidermal growth factor-like domain and binds to ErbB4 receptor, and is useful to prevent or treat NRG3 associated disorders, particularly nerve damage. Abetalipoproteinaemia, Tangier disease, Krabbe's disease, Metachromatic leukodystrophy, Fabry's disease and Dejerine-Scottas syndrome. This is the amino acid sequence of the novel mouse neuregulin related ligand /note= "Extracellular epidermal growth factor-like domain. Specifically claimed in claim 2" .362
 /label= Extracellular domain
 /note= "Specifically Claimed in claim 5" 288. .334 /label= EGF-like_domain Location/Qualifiers Example 1; Fig 4A-B; 60pp; English. Zhang D; 2001US-00817647. 98US-00107979. 97US-0053641P Mark MR, (GETH) GENENTECH INC WPI; 2002-617760/66. N-PSDB; ABK90728. US2002082229-A1. Sequence 713 AA; 26-MAR-2001; 30-JUN-1998; Godowski PJ, 24-JUL-1997; 27-JUN-2002 Domain Domain (NRG3)

Gaps 0 100.0%; Score 47; DB 5; Length 713; 100.0%; Pred. No. 3.8e-40; 1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47 0; Indels 100.0%; Prec. ... Query Match
Best Local Similarity 100.0.
The 47; Conservative

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288 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCREGYQGVRCDQFL 334

RESULT 13 AAW97618

ò g AAW97618 standard; protein; 720 AA. 10-MAY-1999 (first entry) AAW97618;

Neuregulin related ligand; NRG3; hNRG3B1; human; ErbB4 receptor; signal transduction; nervous system disorder; neurodegeneration; neuropathy; therapy; diagnosis.

Human neuregulin related ligand NRG3

us-09-107-979-4.olig.rag

screening

Homo sapiens.

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This is the amino acid sequence of human neuregulin related ligand NRG3, a novel member of the epidermal growth factor (EGF)-like family of a novel member of the epidermal growth factor (EGF)-like family of protein ligands that binds to the ErbB4 receptor, but not to the ErbB2 or ErbB3 receptor, and which activates ErbB4 receptor, tyrosine phosphorylation. The sequence was deduced from the nucleotide sequence of a cDMA clone (see AAXO588) from a foetal brain library. The EGF-like commain of NRG3 is distinct from those of NRG3 or acDMA clone (see AAXO588) from a foetal brain library. The EGF-like commain of NRG3 is distinct from those of other neuregulins. An alternatively spliced form of human NRG3 is provided in AAW97619. The invention provides human and murine NRG3 is provided in AAW97619. The invention of NCG3s. The NRG3 polypeptides (see also AAW97617), expression vectors, host cells and methods for the crecombinant production of NRG3s. The NRG3 polypeptides and in vitro. Complementation of cells having the ErbB4 receptor in vivo and in vitro. They can be used to prevent or treat damage to a nerve or damage to other NRG3-expressing or NRG3-responsive cells, e.g. brain, heart, or kidney cells in particular, they can be used to treat diseases which involve neural cells growth such as demyelination, or damage or loss of glial cells end managed by e.g. trauma, surgery, stroke, malignancy, or toxic agents. NRG3 can also be used to treat motor neuron disorders such as amyotrophic disease, nutritional deficiency, neurodegenerative disorders such as myotrophic lateral sclerosis (Lou Gehrig's disease), neurodegenerative disorders such as surgery strophy or paralysis, neurodegenerative disorders such as surgery strophy or paralysis, neurodegenerative disorders such as shipping spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, pellepsy, multiple sclerosis, Huthington's chorca, pown's cyndrome, nerve deafness, and Menler signated as collected with systemic disease. They dead
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated neuregulin related ligand-3 - used to develop products for treating nervous system disorders, e.g. stroke, ischaemia, infection, malignancy, Alzheimer's disease or Down's syndrome.
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                                                                                                                                                                                         "mucin-like Ser/Thr-rich region, contains sites
                                                                1. .360
'note= "extracellular domain, specifically claimed in
                                                                                                                                                                                                                                                                                                       "transmembrane domain"
                                                                                                                                                                                                /note= "mucin-like Ser/Thr-
for O-linked glycosylation"
                                                                                                                                                  "hydrophobic region"
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                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Zhang D;
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97US-00899437
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                                                                                                       Claim 5(a)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The HLF is involved in the regulation of cell growth. Detection of different levels of expression of the HLF gene can be used for the diagnosis of disorders, e.g. in the neural system. In particular, detection of different levels of HLF gene expression in cells or body fluid of an individual can be used for diagnosing cancer. The products can also be used in the treatment of disorders involving abnormal levels of HLF activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated heregulin-like factor - used to develop products for the diagnosis and treatment of disorders involving regulation of cell growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the human heregulin-like factor (HLF) of the invention.
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                                                                                                                     286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332
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100.0%; Pred. No. 3.8e-40;
iive 0; Mismatches 0;
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100.0%; Pred. No. 3.8e-40;
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                                                                                                                                                                                                                                                                        Human heregulin-like factor sequence.
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                                                               Local Similarity
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                        Sequence 720 AA;
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ABG32065;
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(first entry) 05-NOV-2002

Human novel neuregulin related ligand NRG3B1.

autonomic neuropathy; hereditary neuropathy; Charcot-Marie-Tooth disease; Refsum's disease; Abetalipoproteinaemia; Tangier disease; Krabbe's disease; Metachromatic leukodystrophy; Fabry's disease; Dejerine-Scottas syndrome; human; gene; ss; NRG3B1. Neuregulin related ligand; NRG3; neuroprotective; cell therapy; epidermal growth factor-like domain; EGF-like domain; Bell's palsy; Exb8 receptor detection; amyotrophic lateral sclerosis; paralysis; lou Gehrig's disease; spinal muscular atrophy; multiple sclerosis; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; epilepsy; Huntingdon's chorea; Down's syndrome; nerve deafness; Meniere's disease; neuropathy; distal sensorientor neuropathy;

Homo sapiens.

Location/Qualifiers Key Domain Domain

1. .360 /label= Extracellular domain /label= Specifically claimed in claim 5" 286. -332 /label= EGF-like domain /note= "Extracellular epidermal growth factor-like domain"

US2002082229-A1

27-JUN-2002

26-MAR-2001; 2001US-00817647.

97US-0053641P. 98US-00107979 24-JUL-1997; 30-JUN-1998;

(GETH) GENENTECH INC

Zhang D; Godowski PJ, Mark MR,

WPI; 2002-617760/66. N-PSDB; ABK90731 A new neuregulin related ligand designated NRG3 has an epidermal growth factor-like domain and binds to ErbB4 receptor, and is useful to prevent or treat NRG3 associated disorders, particularly nerve damage.

Example 1; Fig 4A-B; 60pp; English.

The invention describes a polypeptide comprising an amino acid sequence encoding an epidermal growth factor (EGF)-like domain, and having the binding characteristics of neuregalian related ligand (MRG3) and bolypeptide can be used to detect ErbB# receptor in a mammalian tissue sample, and also to prevent or treat disorders associated with NRG3 such as important lears a sclerosis (lou Gehrig's disease), Bell's palsy and various conditions involving spinal muscular atrophy or paralysis, neurodegenerative disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, Huntingdon's chorea, Down's syndrome, nerve deafness, Meniere's disease, neuropathy such as distall sensorimotor neuropathy or autonomic neuropathy, hereditary neuropathies such as charcot-Marie-Tooth disease, Refsum's disease, Metachromatic conditions and page of the novel human neuregulin related ligand conditions.

Sequence 720 AA;

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                                         0;
ch 100.0%; Score 47; DB 5; Length 720; l Similarity 100.0%; Pred. No. 3.88-40; 47; Conservative 0; Mismatches 0; Indels
Query Match
Best Local Similarity
Matches 47; Conserv
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1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 47	286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332	
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Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

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2, 2004, 13:11:24; Search time 193 Seconds (without alignments) 140:117 Million cell updates/sec

US-09-107-979-4
277
1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL 47

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB s Maximum DB s

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

UniProt_02:*
1: uniprot sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	11 12 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			Orycrola	u	035947 mesocricetu					rattus	anna mis			110		c	Dariotas monto sapi	OIIIOIII OIIIOIII	TIOIIIO		Caclos nomo saplen		TIOMO	Diomo Pond	Omort	SILLIS	Osberze mus musculu	200	E CHILLS		
SUMMARIES	ΩΙ	NRG3 MOUSE		NRG1 XENLA	Q6TGK9	AAR00250	035947	Q7RTW1	NRG1 HUMAN	Q7RTV8	Q9ESA9	Q9ESB0	NRG4 MOUSE	NRG4 HUMAN	Q6PK <u>6</u> 1	O7RTWO	007112	AAH06492	SMDF HIMAN	061075	C7RTW2	O961B3	CAG29284	07RTV9	OZRTW3	O7RTW4	NRG2 MOTISE	081080	08BX76	060898	OEDR99	Q9ESA8	
	DB						7										7						N			N	-	0	1 (1	7	~	7	
	Query Match Length	7	720	677	394	394	461	462	639	640	298	695	115	115	241	241	241	241	296	296	296	296	296	422	637	645	756	76	296	645	700	111	
ф	Query	100.0	100.0	L)	41.0	41.0	т.	м.	41.0	•		40.3	39.7	39.4	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.7	37.5	37.4	7	37.4	37.4	37.0	
	Score	277		126.5	113.5	113.5	113.5	•^ ი	113.5	113.5	111.5	111.5	110	109	104.5	104.5	104.5	104.5	104.5	104.5	104.5	104.5	104.5	104.5	104.5	104.5	104	103.5			103.5		
	Result No.	н	2	M	4	2	1	~ (30 (י ת	0 1	7	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	

	O9esa3 rattus norv	rattus	Q9esal rattus norv	P43322 r pro-neure		Ogesas rattus norm	Oglman lumpir akin	005199 Gallas	Olding anombolog a		On 1469 Gaenowhahai	Q90y54 brachydanio
Q9ESA7 O9FSA6	Q9ESA3	Q9ESA2	Q9ESA1	NRG1 RAT	Q9ESB1	Q9ESA5	091MZ0	NRG1 CHICK	070 <u>10</u> 6	0810X1	001768	JAG3_BRARE
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136	317	323	342	662	700	782	83	602	797	54	2192	1213
37.0	37.0	37.0	37.0	37.0	37.0	37.0	35.7	35.6	35.4	35.0	33.4	33.0
102.5	102.5	102.5	102.5	102.5	102.5	102.5	66	98.5	96	97	92.5	91.5
32	34	32	9 1	3.7	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT NRG3 M	Juse
AC AC	STZ
다 다 다 다	16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update)
DE DE	ulin-3 precursor
OS GN	Name=Nrg3; Mus musculus (Mouse).
88	Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
N. N.	
R.P.	SEQUENCE FROM N.A. IISSUE-Brain:
RX RA	720; PubMed=9275162;
R.A	Hillan K., Crowley C., Brush J., Godowski P.J.;
RI	"Neuregulin-3 (NRG3): a novel neural tissue-enriched protein that binds and activates ExbB4 ".
RL	Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).
98	e kinase receptor
ខ្លួ	activation of the receptor. Does not bind to the RGF receptor,
38	1
5 6	a proteolytically released soluble growth factor form. The
ខ្លួ	membrane-bound form does not seem to be active (By similarity). -1- IISSUE SPECIFICITY: Expressed in symmatheric motor and concom-
ពួក	neurons.
ខ្លួ	
25	brain, spinal cord, trigeminal, vestibular-cochlear, and spinal
ខ្លួ	ganglia. In adults, expressed in spinal cord, and numerous brain regions.
ຍູເ	may be involved in the
ខ្លួ	or craittening and proceduring processing. Regulation of the proteolytic processing involves initial intracellular domain
មួម	
ည္မ	
ខ្លួ	-!- PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the column for
ខ្លួ	form
រូបូ	 -:- FIM: Extensive glycosylation precedes the proteolytic cleavage (By similarity).
ပ္ပင္ပ	SIMILARITY:
38	,
ខ្លួ	hrough a
g	the European Bioinformatics Institute. There are no restrictions on its

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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         R PTR; T4444/; 1.1...
R PTR; T4444/; 1.1...
R MGJ; MGI:1097165; Nrg3.
R MGJ; MGI:1097165; Nrg3.
R MGJ; MGI:1097165; Nrg3.
R MGJ; MGI:1097165; F:protein binding; IPI.
R GO; GO:0007243; F:protein kinase cascade; IDA.
BR GO; GO:000742; EGF_2.
BR InterPro; IPR006209; EGF_1ike.
BR InterPro; IPR00639; EGF_1ike.
BR PFam; PF00158; Neuregulin.
BR PFGAITE; PF00168; EGF_2: 1.
BR PROSITE; PS01186; EGF_2: 1.
BR PROSITE; PS0126; EGF_3: 1.
The Properties of the factor; Multigene family; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pro-neuregulin-3 precursor (Pro-NRG3) [Contains: Neuregulin-3 (NRG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                Extracellular (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Ser/Thr-rich.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            9F7D1D5E7FC8DCF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 277; DB 1, 100.0%; Pred. No. 1e-25; ative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                    Poly-Ala.
Poly-Thr.
Poly-Ala.
Poly-Ser.
Poly-Thr.
Py similarity.
By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                EGF-like.
                                                                                                                                                                                                                                                                                                           Poly-Ala.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last seqn
05-JUL-2004 (Rel. 44, Last anno
                                                          EMBL; AF010130; AAB70914.1; -.
PIR; T44447; T44447.
                                                                                                                                                                                                                                                                                                                                                                                                             77369 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                 135
253
263
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361
362
383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                   321
713 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRG3 HUMAN
P56975;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=NRG3;
                                                                                                                                                                                                                                                      DOMAIN
TRANSMEM
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DISULFID
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DOMAIN
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NRG3 HUMAN
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ERBEZ OF ERBES receptors.

-!- SUBCELLULAR LOCATION: Exists as an type I membrane protein and as a proteolytically released soluble growth factor form. The a proteolytically released soluble growth factor form. The a proteolytically released soluble growth factor form. The respection of corpus callosum. Expressed at lower level in with the exception of corpus callosum. Expressed at lower level in testine, Not detected in heart, placenta, lung, liver, skeletal muscle, kidney, pancreas, spleen, thymus, prostate, ovary, small intestine, colon and peripheral blood leukocytes.
-!- DOMAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing. Regulation of the proteolytic processing involves initial intracellular domain dimerization (Expressing the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor protein tyrosine kin. . .; NAS. cell growth; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  form (By similarity). 
 -!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 domain (By similarity).
-!- PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pro-neuregulin-3, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIN, 605533; -.

R GO, GO:0005576; C:extracellular; NAS.

R GO; GO:0005877; C:integral to plasma membrane; NAS.

R GO; GO:0005877; C:integral to plasma membrane; NAS.

R GO; GO:0001558; F:growth factor activity; NAS.

R GO; GO:0001558; F:regulation of cell growth; NAS.

R GO; GO:0007170; P:transmembrane receptor protein tyrosine kin. . .;

R GO; GO:0007170; P:transmembrane receptor protein tyrosine kin. . .;

R InterPro; IPR00620; BGF_2.

R InterPro; IPR006210; IEGF_2.

R InterPro; IPR0062154; Neuregulin.

R Pfam; PF00008; BGF; 1.

R Pfam; PF000158; Neuregulin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neuregulin-3.
Extracellular (Potential).
Internal signal sequence (Potential).
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PROSITE; PS0022; EGF 1; 1.
PROSITE; PS01186; EGF 2; 1.
PROSITE; PS50026; EGF 3; 1.
EGF-like domain; Growth factor; Multigene family; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity.
A4D6F10DDB95A693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytoplasmic (Potential).
Ser/Thr-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: Belongs to the neuregulin family.
-!- SIMILARITY: Contains 1 EGF-like domain.
HSSP; P01133; 1JL9.
HGNC:7999; NRG3.
MIM, 605533; --
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Poly-Thr.
By similarity.
By similarity.
By similarity.
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0; Mismatches
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720 AA;
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nes 47; Conserv
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ID NRG1 XENLA
AC 093383; Q9W6N0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       361
382
105
286
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DOMAIN
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                                                           <u>-</u>
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(By

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Isold=093383-1; Sequence=Displayed;
Name=CRD: Synonyms=CRD-NRG1, Cysteine rich domain;
Isold=093383-1; Sequence=VSP 00349, VSP 003450;
-!-TISSUE SPECIFICITY: Isoform alphal is expressed in brain and muscle. Isoform CRD is expressed in brain and spinal cord, but at very low level in muscle.
-!-DOMAIN: TARGE: Strong expressed in the myotomal muscle. Spinal cord of the embryo. Also expressed in the myotomal muscle.-!-DOMAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing. Regulation of the proteolytic processing. Regulation of the dimerization (By similarity).
-!-DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its was by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-99316087; PubMed-10183827;
Yang J.F., Zhou H., Choi R.C., Ip N.Y., Peng H.B., Tsim K.W.K.;
"A cysteine-rich form of Xenopus neuregulin induces the expression of moctylcholine receptors in cultured myotubes.";
MOI. Cell. Neurosci. 13:415-429(1999).
-- FUNCTION: Direct ligand for the ERBB tyrosine kinase receptors.
Induces expression of acetylcholine receptor in synaptic nuclei.
-- SUBCELLULAR LOCATION: Exists as a type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- PTM: Extensive glycosylation precedes the proteolytic cleavage (By
similarity).
                                                                                                                                                                                                                                                                          Yang J.F., Zhou H., Pun S., Ip N.Y., Peng H.B., Tsim K.W.K.; "Cloning of cDNAs encoding xenopus neuregulin: expression in myotomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist. Isoforms have alpha-
or beta-type EGF-like domains;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
  16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pro-neuregulin-1 precursor (Pro-NRG1) (Contains: Neuregulin-1)
                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM ALPHA1), AND ALTERNATIVE SPLICING. MEDLINE=98352126; Pubmed=9685585;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Contains 1 EGF-like ŏomain.
-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: Belongs to the neuregulin family.
                                                                                                                                                                                                                                                                                                                                             Brain Res. Mol. Brain Res. 58:59-73 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (Se or send an email to license@isb-sib.ch).
                                                                                                        Xenopus laevis (African clawed frog)
                                                                                                                                                                                                                                                                                                                         embryo development
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM CRD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPRO00742; EGF 2.
InterPro; IPR006209; EGF like.
InterPro; IPR007110; Ig-like.
InterPro; IPR002154; Neuregulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AF076618; AAC26804.1; -.
EMBL; AF142632; AAD33893.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00008; EGF; 1.
                                                                                                                                                                      Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q12780; 1HRE.
                                                                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Alphal
                                                                                                                                                                                                                                                                                                                           muscle during
                                                                                      Name=NRG1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain.
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NDTVTVNVTIVPK -> MSEDTAEGLQNQCSEQSSOPPSAE
CHORESMPETOBEERTHYGITICATTCCVCLBADRLRICIN
SEX.CI.PPILACI.ISLCLCIAGLKWVFVDKIPEYDSPTHLD
PGHRQQDLILYTDTAESTLVPSSVRTLPVIIPTTDSSRAVY
                                                                                                                                                                                                                                                                   N-linked (GlcNAc. .) (Potential).
MAEKKKVKEGKGRKGRKGKCKCKAEGSDQGAAASPKLKE
                                                                                                                                                                                                                                                                                        IKTQSVQEGKKLVLKCQAVSEQPSLKFRWFKGEKEIGAKNK
PDSKPEHIKIRGKKKSSELQISKASSADNGEYKCMVSNQLG
                             PROSITE, P600022; EGF 1, PROSITE; P600022; EGF 1, PROSITE; P800186; EGF 2; 1. PROSITE; P850026; EGF 3; 1. PROSITE; P850026; EGF 3; 1. Alternative splicing; EGF-like domain; Glycoprotein; Growth factor; Immunoglobulin domain; Transmembrane. CHAIN 1 259 Pro-neuregulin-1 (By similarity). Pro-neuregulin-1, membrane-bound form (GTAIN)
                                                                                                                                         Internal signal sequence (Potential).
Cytoplasmic (Potential).
[19-11ke C2-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryctólagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                           Lys-rich.
N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 45.7%; Score 126.5; DB 1; Length 677; l Similarity 43.5%; Pred. No. 4.4e-07; 20; Conservative 10; Mismatches 15; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                KPGFTGARCTETDPLRVVRSEKHLGIEFME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                            RCQNYVMASFYK (in isoform CRD)
/FTId=VSP_003450.
                                                                                                                                                                                                                                                                                                                                                          FKFGTSLLPTE (in isoform CRD) /FIId=VSP 003449.
                                                                                                                           similarity).
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                 49279E8F5BAE396F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                             By similarity.
By similarity.
By similarity.
By similarity.
                                                                                                                                                                                     EGF-like.
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05-JUL-2004 (TrEMBLrel. 27, Last seque
05-JUL-2004 (TrEMBLrel. 27, Last anno!
Neuregulin 1 alpha isoform (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                 677 AA; 75794 MW;
                      PRINTS; PR01089; NEUREGULIN.
Pfam; PF00047; ig; 1.
Pfam; PF02158; Neuregulin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                      132
232
232
220
231
231
124
130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9986;
                                                                                                                                  DOMAIN
TRANSMEM
DOMAIN
                                                                                                                                                                                 DOMAIN
DISULFID
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                                                                                                                                                                                                                                                               CARBOHYD
VARSPLIC
                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
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Q6TGK9
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Gaps

1;

Pfam; PF00008; EGF; 1

-> PNEFIGD

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Q12780; 1HRE
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    HSSE;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Neuregulin 1 alpha isoform (Fragment).
Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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41.0%; Score 113.5; DB 2; Length 394;
Best Local Similarity 34.8%; Pred. No. 1e-05;
Matches 16; Conservative 14; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                    Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 HLVKCAEKEKTFCVNGGBCFWVKDLSNPSRYLCKCQPGFTGARCTE 214
                                                                                                                                                                                                                                                                                                                                                                                                                                 169 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTE 214
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                                                                                                                                                                                                                                                                                                                                                                                                   1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Velasco J.A., Notario V.; Velasco J.A., Feljoo E., Avila M.A., Notario V.; Submitted (APR-1997) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              Indels
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Hendrickx J.;
Submitted (GEP-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY421758; AAR00250.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            394 AA; 42980 MW; C183EE80927443F9 CRC64;
                                                                                                                                                                                                                                                                             394 AA; 42980 MW; C183EE80927443F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                    Query Match
41.0%; Score 113.5; DB 2;
Best Local Similarity 34.8%; Pred. No. 1e-05;
Matches 16; Conservative 14; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     461 AA
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          Pfam; PF00047; ig; 1.
Pfam; PF02168; Neuregulin; 1.
PRINTS; PF02169; Neuregulin; 1.
SWART; SM00161; EGF; 1.
SWART; SM00408; IG; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS0186; EGF_2; 1.
PROSITE; PS50026; EGF_2; 1.
PROSITE; PS50026; EGF_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U96612; AAB71812.1; -.
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394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9986;
                                                                                                                                                                                                                         EGF-like domain.
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RX Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Sigurdsson T., Ghosh S., Brynjolfsson J., Gunmarsdottir S., Sajmundsson T., Chou T.T., Hjaltason O., Birgisdottir B., Jonsson H., RA Gudnadottir V.G. Gudmundsdottir E., Bjornsson A., Ingwarsson B., A Ingason A., Sigiusson S., Hardardottir H., Harvey R.P., Brunner D., Manolescon T., Gonzalo A., Lemke G., Sainz J., Johannesson G., Andresson T., Gudbjartsson D., Manolescu A., Frigge M.L., Gurney M.E., RY Andresson T., Gudbjartsson D., Manolescu A., Frigge M.L., Gurney M.E., Andresson T., Gudbjartsson B., Manolescu A., Frigge M.L., Gurney M.E., Andresson T., Gudbjartsson H., Stefansson K.; Am. J. Hum. Genet. 71:0-0(2002).

RY Meurequlin I and Susceptibility to Schizophrenia."; Am. J. Hum. Genet. 71:0-0(2002).

C. EMBL/Genbank/DbbJ third party annotation (TPA) entry.

C. G. GO:0005102; Freceptor binding; IEA.

DR GO; GO:0005102; Freceptor binding; IEA.

DR Ffam; PF000110; Ig-like.

DR Pfam; PF00047; ig; 1.

DR PROSITE; PS01085; BGF 1: 1.

DR PROSITE; PS01082; BGF 1: 1.

DR PROSITE; PS01085; EGF 1: 1.

DR PROSITE; PS01085; EGF 1: 1.

DR PROSITE; PS01085; EGF 2: 1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41.0%; Score 113.5; DB 2; Length 461; 34.8%; Pred. No. 1.2e-05; Live 14; Mismatches 15; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ
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Last annotation update)
HSSP; Q12'80; Inter.

G0, G0:0005102; F:receptor binding; IBA.

G0, G0:0005790; P:embryonic development; IEA.

InterPro; IPR006209; EGF_1.

InterPro; IPR006209; EGF_1.

InterPro; IPR00510; IEGF.

InterPro; IPR00110; Ig-like.

INTER; PR01010; Ig-like.

INTER; PR00101; EGF; I.

INTER: PR00116; EGF; I.

INTER: PR0016; IIII6; EGF; I.

INTER: P
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01-MAR-2004 (TrEMBLrel. 26,
01-MAR-2004 (TrEMBLrel. 26,
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Best Local Similarity 34.8%
Matches 16; Conservative
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002237; O14667; P98202; Q02298; Q07110; Q07111; Q12779;

Q12780; Q12781; Q12782; Q12783; Q12784; Q9UPR3;

16-OCT-2001 (Rel. 40, Last sequence update)

16-OCT-2004 (Rel. 40, Last sequence update)

16-OCT-2004 (Rel. 40, Last amnotation update)

PO-neuregulin-1 precursor (Pro-NRGI) [Contains: Neuregulin-1 (Neu differentiation factor) (Heregulin) (HRGO) (Breast cancer cell differentiation factor) (Heregulin) (HRGO) (Breast cancer cell differentiation factor) (Heregulin) (HRGO) (Grast cancer cell differentiation factor) (Heregulin) (HRGO) (Grast cancer cell differentiation factor) (Heregulin) (HRGO) (Grast cancer cell differentiation factor) (Glast growth
                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS 1; 6; 7 AND 8), AND PARTIAL SEQUENCE. MEDLINE=92271253; PubMed=1350381; Holmes W.E., Sliwkowski M.X., Akita R.W., Henzel W.J., Lee J., Park J.W., Yansura D., Abadi N., Raab H., Lewis G.D., Shepard H.M., Kuang W.-J., Wood W.I., Goeddel D.V., Vandlen R.L.; Ildentification of heregulin, a specific activator of pl85erbB2."; Science 256:1205-1210(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 2; 3; 4; 6; 7 AND 8).

TISSUB=Kidney adenocarcinoma, and Pituitary;

MEDLINE=94188683, PubMed=7509448;
Wen D., Suggs S.V., Karunagaran D., Liu N., Cupples R.L., Luo Y., Janssen A.M., Ben-Baruch N., Trollinger D.B., Jacobsen V.L., Meng S.-Y., Lu H.S., Hu S., Chang D., Yang W., Yanigahara D., Koski R.A., Yarden Y.;

"Structural and functional aspects of the multiplicity of Neu differentiation factors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marchionni M.A., Goodearl A.D.J., Chen M.S., Bermingham-McDonogh Kirk C., Hendricks M., Danehy F., Misumi D., Sudhalter J., Kobayashi K., Wroblewski D., Lynch C., Baldasarre M., Hiles I., Davis J.B., Hsuan J.J., Totty N.F., Otsu M., McBurney R.N., Waterfield M.D., Stroobant P., Gwynne D.; "Glial growth factors are alternatively spliced erbB2 ligands expressed in the nervous system.";
                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=92208945; PubMed=1348215;
Peles E., Bacus S.S., Koski R.A., Lu H.S., Wen D., Ogden S.G.,
                                                                DB 2; Length 462;
                                                                                                                                                             45
                                           Score 113.5; DB 2; Leus-
Pred. No. 1.2e-05;
                                                                                                                                    1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ
                    50848 MW; 8CAADBB30056A80D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. OF GAMMA-HEREGULIN FUSION PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=NRG1; Synonyms=HGL, NDF, HRGA, GGF, SMDF;
                                                                                                   14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 8 AND 9).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=93205115; PubMed=8096067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Breast cancer;
MEDLINE=97472144; PubMed=9333014;
                                                            41.0%;
34.8%;
  PS50835; IG_LIKE;
                                                                                                 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 362:312-318(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 69:205-216(1992)
                      462 AA;
                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
PROSITE;
SEQUENCE
                                                          Query Match
                                                                                                 Matches
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RX PROCTURE BY NAR OF 175-241 (ISOFORM 1).

RX MADGIANE-9341264; PubMede9605829;

RA Magata K., Kobda D., Hatanaka H., Ichikawa S., Matsuda S.,

RA Magata K., Kobda D., Hatanaka H., Ichikawa S., Matsuda S.,

RA Yamamoto T., Suzuki A., Inagaki F.,

RT "Solution structure of the epidermal growth factor-like domain of

RA PAGATIAN-1253 (1994).

REMBO J. 13:3517-3523 (1994).

CC -:- FUNCTION: Direct ligand for pl80erbB-4.";

REMBO J. 13:3517-3523 (1994).

CC -- TUNCTION: Direct ligand for pl80erbB-4.";

CC -- FUNCTION: Direct ligand for BRBB3 and ERBB4 tyrosine kinase

resulting in ligand-stimmlated tyrosine phosphorylation and

diverse functions such as inducing growth and differentiation of

epithelial, glial, neuronal, and skeletal muscle cells; inducing

cc activation of the neuromascular junction; stimulating

and inducing differentiation of mammary tumor cells; stimulating

command and inducing differentiation of mammary tumor cells; stimulating

and inducing differentiation of mammary tumor cells; stimulating

conformation of the neuromascular junction; stimulating

and inducing differentiation of mammary tumor cells; stimulating

conformation of the neuromascular junction in the mammary gland

and inducing differentiation of mammary tumor cells; stimulating

conformation of the mammary tumor cells; stimulating

comment—ALTERNATIVE PRODUCTS;

comment—Addition! seem to seem to be active. The secreted

isoform 9 has a signal peptide. The isoform 8 may be nuclear.

comment—Additional isoforms seem to exist. Isoforms with

a lg domain but no glycosylation domain, isoform 8 may be nuclear.

Isold—CO2297-1; Sequence—Co2297-1; Sequence—Co2297-1; Sequence—Co2297-1; Sequence—Co2397-1; Sequence—Co2397-1; Sequence—Co2397-1; Sequence—Co2397-1; Sequence—Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20065180; PubMed=10597312;
Liu X., Baker E., Eyre H.J., Sutherland G.R., Zhou M.;
Gamma-heregulin: a fusion gene of DOC-4 and neuregulin-1 derived from
a chromosome translocation.";
Oncogene 18:7110-7114(1999).
                                                                                                                                                                                                                                                                     MEDINE=9336731; PubMed=7689552;
Culouscou J.-M., Plowman G.D., Carlton G.W., Green J.M., Shoyab M.;
"Characterization of a breast cancer cell differentiation factor that
specifically activates the HER4/pl80erbB4 receptor.";
J. Biol. Chem. 268:18407-18410(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99455251; PubMed=10523851; Wang X.-Z., Jolicoeur E.M., Conte N., Chaffanet M., Zhang Y., Wang X.-Z., Jolicoeur E.M., Conte N., Chaffanet M., Zhang Y., Mozziconacci M.-J., Feiner H., Birnbaum D., Pebusque M.-J., Ron D.; "Gamma-heregulin is the product of a chromosomal translocation fusing the DOC4 and HGL/NRG1 genes in the MDA-MB-175 breast cancer cell
"Gamma-heregulin: a novel heregulin isoform that is an autocrine growth factor for the human breast cancer cell line, MDA-MB-175."; 661
                                                                                                                                                        Schoumacher F., Herzer S., Flury N., Kueng W., Mueller H.,
                                                                                                                                                                                                     Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=3; Synonyms=Alpha2B;
IsoId=002297-3; Sequence=VSP_003434, VSP_003435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=2; Synonyms=Alpha1A,
Isold=002297-2; Sequence=VSP_003431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oncogene 18:5718-5721 (1999).
                                                                                                                           SEQUENCE OF 1-210 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                 CHROMOSOMAL TRANSLOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOSOMAL TRANSLOCATION
                                                                                                                                                                                                                                                    SEQUENCE OF 19-27.
                                                                                                                                                                               Eppenberger U.;
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VSP_003426, VSP_003429,

VSP 003433;

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1- PTM: Extensive glycosylation precedes the proteolytic cleavage (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor
                                                                                        Name=7, 2720.777; Sequence=VSP_003427;
Isold=Q02297-8; Sequence=VSP_003429, VSP_003430;
Isold=Q02297-8; Sequence=VSP_003429, VSP_003426,
Isold=Q02297-9; Sequence=VSP_003425, VSP_003426,
IsoId=Q02297-4; Sequence=VSP_003432,
                      Name=6; Synonyms=Beta1, Beta1A;
IsoId=Q02297-6; Sequence=VSP_00342B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , M94168, AAA30022...,
, U02325, AAA19950.1; -.
, U02326, AAA19951.1; -.
L; U02327, AAA19952.1; -.
L; U02328, AAA19953.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M94165; AAA58638.1; -. EMBL; M94166; AAA58639.1; -. EMBL; M94168; AAA58640.1; -. EMBL; M94168; AAA58641.1; -. EMBL; U02325; AAA19950.1; -.
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AAB59622.1; -.
AAB59358.1; -.
                                                                                                                                                                                                                                             Name=10; Synonyms=SMDF;
                                                                         Name=7; Synonyms=Beta2;
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Best Local Similarity
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EMBL;
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EMBL;
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Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Sigmundsson T., Ghosh S., Brynjolfsson J., Gunnarsdottir S., Ivarsson O., Chou T.T., Hjaltsson O., Birgisdottir B., Jonsson H., Ingason A., Sigfusson S., Hardardottir H., Harvey R.P., Brunner D., Mutel V., Gonzalo A., Lemke G., Sainz J., Johannesson G., Andresson T., Gudpiartrsson D., Manolescu A., Frigge M.L., Gurney M.E., Kong A., Gulcher J.K., Petursson H., Stefansson K.; Wheuregulin I and Susceptibility to Schizophrenia."; M. Schlanskous: The sequence shown here is derived from an EMBL/Genbank/DDBA third party annotation (TPA) entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41.0%; Score 113.5; DB 2; Length 34.8%; Pred. No. 1.7e-05; ive 14; Mismatches 15; Indels
                 177 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPGFTGARCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11AFC54B32527ACC CRC64;
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                                                                                                                                                                    (TrEMBLrel. 26, Last sequence update) (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0009790; P:embryonic development; IEA.
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                                                                                                                                                     01-MAR-2004 (TrEMBLrel. 26, Created)
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PROSITE; PS00022; BGF_1; 1.
PROSITE; PS01186; BGF_2; 1.
PROSITE; PS50026; EGF_3; 1.
PROSITE; PS50835; IG LIRR; 1.
SEQUENCE 640 AA; 70361 MW; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000742; EGF 2.
InterPro; IPR006209; EGF like.
InterPro; IPR007110; Ig-like.
InterPro; IPR002154; Neuregulin.
                                                                                                                                                                                                  Neuregulin 1 isoform HRG-alpha
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Pfam; PF02158; Neuregulin; 1.
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                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                        (Human)
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                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                         01-MAR-2004
                                                                                                                                                                                       01-MAR-2004
                                                                                                                                                                                                                        Name=NRG1;
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                                                                                                                         Q7RTV8
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Q9ESA9
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                                                                                        RESULT
Q7RTV8
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Gaps

7;

41.0%; Score 113.5; DB 1; Length 639; 34.8%; Pred. No. 1.7e-05; ive 14; Mismatches 15; Indels 1:

16, Conservative

Matches

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MGD; MGI:1933833; Nrg4.
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                                                                                                                                                                                                                                                                                                                                                                                                           Name=Nrg4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     farden Y
                                                                                                                                                                                                                                                                                                                                                                                   (NRG-4)]
                                                                                                                                                                                                                                                                               D9WTX4;
                                                                                                                                                                                                                                      NRG4 MOUSE
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Mammalia, Eutheria, Rođentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.3%; Score 111.5; DB 2; Length 298; 34.8%; Pred. No. 1.4e-05; Live 13; Mismatches 16; Indels 1;
                                  Carroll S.L., Anderson K.D., Frohnert P.W.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!— SIMILARITY: Contains 1 EGF-like domain.
EMBL, AR19440; AAG38429-1; -.
GO; GO:0005102; F:receptor binding; IEA.
GO; GO:0005109; F:receptor binding; IEA.
InterPro; IPR006209; EGF 2.
InterPro; IPR006209; EGF 1ike.
InterPro; IPR006210; IEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=BDIX;
Carroll S.L., Anderson K.D., Frohnert P.W.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: Contains 1 EGF-like domain.
EMBL; AF194439; AAG28428.1; -.
HSSP; Q12780; 1HRE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 AA; 32851 MW; BD76F014C2B33026 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              695 AA; 75646 MW; 5277F2CBA2FB6878 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO: GO: 0005102; F: receptor binding; IEA.
GO: GO: 0005102; F: receptor binding; IEA.
GO: GO: 0009790; P: embryonic development; IEA.
INCEPTO: IPRO00742; EGF 2.
INCEPTO: IPRO02104; HPT SerP S.
INCEPTO: IPRO02114; HPT SerP S.
INCEPTO: IPRO02114; HPT SerP S.
INCEPTO: IPRO02114; Neuregulin.
Pfam; PF00008; EGF; 1.
PFam; PF00188; Neuregulin.; 1.
PRINTS: PR01089; NEUREGULIN.
PROSITE; PS00108; EGF 1.
PROSITE; PS00108; EGF 1.
PROSITE; PS00108; EGF 2; 1.
PROSITE; PS00186; EGF 2; 1.
                                                                                                                                                                                                                                                              Pfam; PF00008; EGF; 1.
Pfam; PF0158; Neuregulin; 1.
PRINTS; PR01089; BGF; 1.
SMART; SM00181; EGF; 1.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS0026; EGF_3; 1.
PROSITE; PS0026; EGF_3; 1.
PROSITE; PS00289; PTS_HPR_SER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TEMBLrel. 16, 01-MAR-2001 (TEMBLrel. 16, 01-MAR-2004 (TEMBLrel. 26, SMDF neuregulin alpha 2a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 34.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like domain.
SEQUENCE 695 A
                   STRAIN=BDIX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=Nrg1
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A PACTOR A P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Liver;
MEDLINE=99276098; PubMed=10348342;
Harari D., Tzahar E., Romano J., Shelly M., Pierce J.H., Andrews G.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: Low affinity ligand for the ERBB4 tyrosine kinase receptor. Concomitantly recruits ERBB1 and ERBB2 coreceptors, resulting in ligand-stimulated tyrosine phosphorylation and activation of the ERBB receptors. Does not bind to the ERBB1, ERBB2 and ERBB3 receptors.
-!- SUBCELLUIAR LOCATION: Exists as an type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active (By similarity).
-!- ALTERNAINE ROOMCTS:
EVENDEDALIANTALIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9WTX4-1; Sequence=Displayed;
TISSUE SPECIFICITY: Highly expressed in pancreas; weakly expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing. Regulation of the proteolytic processing involves initial intracellular domain dimerization (by similarity).

DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM: Extensive glycosylation precedes the proteolytic cleavage (By
                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain (By similarity).

PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Neuregulin-4: a novel growth factor that acts through the BrbB-4 receptor tyrosine kinase.";
Oncogene 18:2681-2689(1999).
                                                                                                      ;
                                           Length 695;
                                                                                                                                                                                                1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                      16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Event=Alternative splicing; Named isoforms=1;
Comment=At least 3 isoforms may be produced;
                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            similarity).
-!- SIMILARITY: Belongs to the neuregulin family.
-!- SIMILARITY: Contains 1 BGF-like domain.
                                 40.3%; Score 111.5; DB 2
34.8%; Pred. No. 3.3e-05;
iive 13; Mismatches 16
                                                                                                                                                                                                                                                                                                                                                                                            115 AA
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF083067; AAD21874.1; -.
Query Match
Best Local Similarity 34.0%
Local Similarity 34.0%
Local 16, Conservative
                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    012780; 1HRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCBI_TaxID=10090;
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Matches
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                                                                                    -
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RETAUSDESCRY R.L., Feringold E.A., Grouse L.H., Derge J.G.,
RICAUSER R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
RICAUSHOR R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
By Charleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Rephaleton M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
Brownstein M.J., Wockwan P.J., McKernan R.D., Mullahy S.J.,
Rohards S., McGwan P.J., McKernan R.J., Marchan P.J., McKernan R.J., Marchan P.J., Wollalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Richards S., Worley M.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Rhahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Blakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield W. Schein J.E., Jones S.J.M., Marra M.A., Spinch P. A.,
Bud M. Mander M. Mallysis of More than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ή.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
    InterPro; IPR001336; EGF_1.
InterPro; IPR000742; EGF_2.
InterPro; IPR006210; EGF_1.
EnterPro; IPR006210; EGF_1.
PENUTS; PR00008; EGF; 1.
PRINTS; PR00009; EGFF1.
PROSITE; PS00022; EGF 1:
PROSITE; PS0022; EGF 1:
PROSITE; PS0022; EGF_3; 1.
PROSITE; PS0026; EGF_3; 1.
Alternative splicing; EGF_1:
Alternative splicing; EGF_1:
Prometries ps0022; EGF_1:
PROSITE; PS0026; EGF_1:
PS0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last amotation update)
Pro-neuregulin-4, short isoform (Pro-NRG4) [Contains: Neuregulin-4
                                                                                                                                                                                                                                                                               Neuregulin-4.
Extracellular (Potential).
Internal signal sequence (Potential).
Cytoplasmic (Potential).
EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                   23 By similarity.
34 By similarity.
45 By similarity.
39 N-linked (GlonAc. . .) (Potential).
60 N-linked (GlonAc. . .) (Potential).
12743 MW, 989AlE376F857B49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and mouse CDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Low affinity ligand for the ERBB4 tyrosine kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%; Score 110; DB 1; Length 115; 42.2%; Pred. No. 8.1e-06; ive 8; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HEQPCGPRHRSFCINGGICYVIPTIPS--PFCRCIENYTGARCEE 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                        62
83
115
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23
34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRG4 HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=NRG4;
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (NRG-4)]
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                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 13
NRG4_HUMAN
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                  dimerization (By similarity)
-!- DOMAIN: ERBB receptor binding is elicited entirely by the EGF-like
domain (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Extensive glycosylation precedes the proteolytic cleavage (By
        receptor. Concomitantly recruits ERBB1 and ERBB2 coreceptors, resulting in ligand-stimulated tyrosine phosphorylation and activation of the ERBB receptors. Does not bind to the ERBB1, ERBB2 and ERBB3 receptors (By similarity).

BRBB2 and ERBB3 receptors (By similarity).

SUBCELLULAR LOCATION: Exists as an type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active (By similarity).

BOMAIN: The cytoplasmic domain may be involved in the regulation of trafficking and proteolytic processing involves initial intracellular domain proteolytic processing involves initial intracellular domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                              -!- PTM: Proteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor form (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pro-neuregulin-4, membrane-bound form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Internal signal sequence (Potential). Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Potential).
Concomitantly recruits ERBB1 and ERBB2 coreceptors,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001336; BGF 1.
InterPro; IPR000742; BGF 2.
InterPro; IPR0006209; BGF 2.
Pfam; PF000008; BGF; 1.
PROSTTE; PS00108; BGF 1; 1.
PROSTTE; PS01186; BGF 2; PALSE_NBG.
PROSTTE; PS01186; BGF 3; 1.
BGF-11ke domain; Glycoprotein; Growth factor; Multigene family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39.4%; Score 109; DB 1; Length 115; 42.2%; Pred. No. 1.1e-05; ive 7; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neuregulin-4.
Extracellular (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .linked (GlcNAc. . .) (P. 72F962E2D0F37AC3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Neuregulin 1, isoform HRG-beta3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similarity).
-!- SIMILARITY: Belongs to the neuregulin family.
-!- SIMILARITY: Contains 1 EGF-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
By similarity.
By similarity.
N-linked (GlcNAc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGF-like.
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05-JUL-2004 (TrEMBLrel. 27, Created)
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61
62
83
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
84
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TRANSMEM
DOMAIN
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Best Local 1
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us-09-107-979-4.rup

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PubMed=12145742;
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             qq
                                                                       A Table Foundary School E. A., Grouse L. H., Derge J. G.,

A Rausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,

A Rausberg R. L., Feingold E. A., Grouse L. H., Derge J. G.,

A Altschul S. F., Collins F. S., Wagner L., Shemen C. M., Schuler G. D.,

RA Altschul S. F., Zeeberg B., Buetow K. H., Schaefer C. F., Bhar N. K.,

A Altschul S. F., Jordan H., Moore T., Max S. I., Wang J., Hisieh F.,

B Diatchenko L., Marusina K., Farmer A. A., Rubin G. M., Hong L.,

RA Brownstein M. J., Usdin T. B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S. S., Loquellano N. A., Peters G. J., Abramson R. D., Mullahy S. J.,

R Richards S. Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,

R Richards S. Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,

R Richards S. Worley K. C., Hale S., Garcia A. M., Gay L. J., Hulyk S. W.,

R Richards S. Worley R. W., Sodergren E. J., Lu X., Gibbs R. A.,

Rahay J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

R Blakesley R. W., Touchman J. W., Green E. D., Dickson M. C.,

R Rodriguez A. C., Grimwood J., Schmutz J., Myers R. M., Butterfield Y. S.,

R Jones S. J., Marra M. A.;

"Generation and initial analysis of more than 15,000 full-length human
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB-OVATY;

A Strausberg R.;
Strausberg R.;
Submitted (ARR-2001) to the EMBL/GenBank/DDBJ databases.
L SIMILARITY: Contains 1 EGF-like domain.
EMBL; BC006492; AAH06492.1; -..
InterPro; IPR00742; EGF 2.
R InterPro; IPR006210; IEGF.
R InterPro; IPR00529; IG.
R InterPro; IPR00529; IG.
R InterPro; IPR00510; IGGF.
R InterPro; IPR00110; IgGF.
R InterPro; IPR00110; IgGF.
R InterPro; IPR00189; Ig.
R EMBRT; SM0008; EGF; 1.
SMART; SM00409; IG; 1.
SMART; SM00409; IG; 1.
R SMART; SM00409; IG; 1.
R PR0SITE; PS00022; EGF 1; UNKNOWN 1.
R PROSITE; PS00025; EGF 1; UNKNOWN 1.
R PROSITE; PS00026; EGF 3; 1.
R PROSITE; PS00028; IG_IIKE; 1.
R EGF-like domain.
SEQUENCE 241 AA; 26114 MW; FEBB9FDF71B816B1 CRC64;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2004 (TrEMBLrel. 26, Created)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Neuregulin 1 isoform GGF (Neuregulin 1 isoform hrg-beta3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.7%; Score 104.5; DB 2
31.2%; Pred. No. 8.3e-05;
tive 14; Mismatches 18
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                                                                                                                                                                                                                                                                                                                                                                                            and mouse cDNA sequences."
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Best Local Similarity 31.2%
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                               FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                    NCBI_TaxID=9606;
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                                                 SEQUENCE
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1,
Stefansson H., Sigurdsson E., Steinthorsdottir V., Bjornsdottir S., Sigurdsson T., Ghosh S., Brynjolfsson J., Gunnarsdottir S., Uvarsson O., Chou T.T., Hjalteson O., Brynjolfston B., Jonsson H., Gudnaddttir V.G., Gudmundsdottir E., Bjornsson A., Ingvarsson B., Ingason A., Sigfusson S., Hardardottir H., Harvey R.P., Brunner D., Mutel V., Gonzalo A., Lemke G., Salnz J., Johannesson G., Andresson T., Gudbjartsson D., Manolescu A., Frigge M.L., Gurney M.E., Kong A., Gulcher J.R., Petursson H., Stefansson K., "Neuregulin I and Susceptibility to Schizophrenia.";
Am. J. Hum. Genet. 71:0-0 (2002).

-- MISCELLANBOUS: The sequence shown here is derived from an EMBI-Genbank/DDBJ third party annotation (TPA) entry.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKH-CRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; Prucuc, 19, 1.
Pfam; Prococ, 19, 1.
Pfam; Procococ, 19, 1.
PROSITE; PS50026; EGF 1; UNKNOWN 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: November 2, 2004, 13:27:39 Job time : 195 secs
                                                                                                                                                                                                                                                                                                                                                          EMBL, BK000383, DAA00046.1, InterPro; IRR000742, EGF 2. InterPro; IRR006209, EGF 1. InterPro; IRR007110, Ig-like. PF00008, EGF, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 31.2
Matches 15; Conservative
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		e ^r

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

November 2, 2004, 13:19:14; Search time 38 Seconds (without alignments) 119.005 Million cell updates/sec

US-09-107-979-4

1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

Database

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

S Description	i	neurogurii-3 [limbo		n	new differentiatio		neu differentiatio	herequlin precurso	glial growth facto	sensorv/motor neur	glial growth facto	herequitin precurso	herequlin. splice	neu differentiatio	neu differentiatio		acetylcholine rece	hypotherical prote		kinase	kinase	growth factor - ra	_	epireonlin - rat	epiredulin precurs	Notch homolog Motor	notch-1 protein -	hetarellilin predi	growth factor - my
Ω	T44447	I38405	I38404	A43273	161719	S62676	I38408	D43273	832359	A56943	S32357	C43273	B43273	A56210	161718	I61722	A45769	T29764	JC5700	JC5702	JC5701	EGVZSF	A56136	JT0747	S68401	A48825	A46019	A37408	EGVZM1
DB	10	ι (1	7	7	7	N	7	N	N	C)	N	7	7	C)	N	N	~	~	~	7	7	-	7	7	~	N	N	N	н
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ery	100.0	41.0	41.0	41.0	40.3	38.1	•	37.7	7	37.7	37.7	37.7	37.7	37.0	37.0	37.0	35.6	33.4	32.5	32.5	32.5	30.7	30.5	30.0	30.0	30.0	30.0	29.8	29.6
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Result No.		7	m	4	Ŋ	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

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Gaps

Ouery Match
Best Local Similarity 34.8%; Pred. No. 5.9e-06;
Matches 16; Conservative 14; Mismatches 15; Indels 1

1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45

à qq

probable EGF-like	hetacellulin precu	hypothetical profe	growth factor - va	growth factor - va	growth factor - va	transforming growt	transforming growt	transforming growt	notch protein homo	epidermal growth f	DELTA-1ike 1 - mon	Noteth homolog prot	hypothetical prote	E-selectin - pig
A44074	JC1467	T27317	WMVZ9	T30766	WMVZ3C	\$27195	WFRTI	I57497	S18188	EGHU	148324	T30201	T25933	JC5092
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230	178	907	140	140	142	159	159	159	2531	1207	722	2352	1372	482
29.6	29.1	28.9	28.7	28.7	28.7	28.7	28.7	28.7	28.5	28.2	28.0	28.0	27.6	27.4
82	80.5	80	79.5	79.5	79.5	79.5	79.5	79.5	79	78	77.5	77.5	76.5	16

ALIGNMENTS

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C;Accession: T44447
R;Zhang, D.; Sliwkowski, M.X.; Mark, M.; Frantz, G.; Akita, R.; Sun, Y.; Hillan, K.; Crov Proc. Natl. Acad. Sci. U.S.A. 94, 9562-9567, 1997
A;Title: Neuregulin-3 (NRG3): A novel neural tissue-enriched protein that binds and actin A;Reference number: Z22773; MUID:97420720; PMID:9275162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:035181; EMBL:AF010130; NID:92429163; PIDN:AAB70914.1; PID:922, C;Genetics: NRO3
C;Genetics: NRO3
C;Superfamily: mouse neuregulin-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 08-Sep-2002
C; Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 08-Sep-2002
R; Mccession: 13405
R; Mccession: 13405
A; Reference number: Assolutional aspects of the multiplicity of Neu differentiation factors (man)
A; Reference number: Assolutional aspects of the multiplicity of Neu differentiation factors (man)
A; Reference number: Assolutional multiplicity of Neu differentiation factors (man)
A; Reference number: Assolutional multiplicity of Neu differentiation factors (man)
A; Reference number: Assolutional multiplicity of Neu differentiation factors (man)
A; Reference number: Assolutional multiplicity of Neu differentiation factors (man)
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neuregulin-3 [imported] - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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A;Molecule type: mRNA
A;Residues: 1-125 *RES>
A;Residues: 1-125 *RES>
A;Cross-references: EMBL:U02327; NID:g408404; PIDN:AAA19952.1; PID:g408405
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
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100.0%; Score 277; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 6.9e-24;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47
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                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA
A;Residues: 1-713 <ZHA>
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Cispecies: Rattus norregicus (Norway rat)
Cispecies: Rattus norregicus (Norway rat)
Cipate: 29-May-1998 #sequence revision 29-May-1998 #text change 09-Jul-2004
Cipate: 29-May-1998 #sequence revision 29-May-1998 #text change 09-Jul-2004
Cipatession: 161719, 161723, 161724; A38220
R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.; Mol. Cell. Biol. 14, 1909-1919, 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa A;Reference number: A66210; MUID:94158863; PMID:7509448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Residues: 1-639 < RES.
A, Residues: 1-639 < RES.
A, Recession: 161723
A, Rocession: 161723
A, Residues: preliminary; translated from GB/EMBL/DDBJ
A, Residues: preliminary; translated from GB/EMBL/DDBJ
A, Residues: 1-639 < RES.
A, Residues: 1-639 < RES.
A, Cross-references: EMBL: U02323; NID: 9408396; PIDN: AAA19948.1; PID: 9408397
A, Accession: 161716
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A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Status: 1-422 «RE5>
A; Residues: 1-422 «RE5>
A; Residues: 1-422 «RE5>
A; Cross-references: EMBL: U02324; NID: 9408398; PIDN: AAA19949.1; PID: 9408399
A; Cross-references: EMBL: U02324; NID: 9408398; S.V.; Bacus, S.S.; Luo, Y.; Trail, G.; Hu, S., Cell 69, 559-572, 1992
A; Title: Neu differentiation factor: a transmembrane glycoprotein containing an EGF doma A; Reference number: A38220; MUID: 92257596; PMID: 1349853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heregulin isoform alpha 2 - human (fragments)
NyAlternate names: differentiation factor neu isoform alpha 2
G'Species: Homo sapiens (man)
C'Species: Homo sapiens (man)
C'Accession: $62676
C'Accession: $62676
C'Accession: $62676
C'Accession: $62676
A'file: Isolation and structural characterization of recombinant human neu differentia A, Reference number: $62676; MUID: $6139341; PMID: $8547341
A, Accession: $62676
A, Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-422,'H','NL',637-638,'ELRRNKAYRSKCMQIQLSATHLRPSSITHLGFIL' <RE4>
A;Cross-references: EMBL:U02317; NID:g408384; PIDN:AAA19942.1; PID:g408385
A;Accession: 161724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rosidues: 1-422, 'H', NL', 637-638, 'ELRRNKAYRSKCMQIQLSATHLRPSSITHLGFIL' <RE
A;Ross-references: EMBL:U02316; NID:g408382; PIDN:AAA19941.1; PID:g408383
A;Accession: I61717
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Residues: 1-422 < WEN>
A;Note: sequence extracted from NCBI backbone (NCBIN:101767, NCBIP:101768)
C;Superfamily: human heregulin; BGF homology; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16; Conservative
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Matches 16; Conserv
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C,Superfamily: human heregulin; EGF homology; i
C,Keywords: alternative splicing; glycoprotein
F,182-221/bomain: EGF homology <EGF>
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Best Local Similarity
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glial growth factor - human
Cispecies: Homo sapiens (man)
Cjate: 02-Dec.1993 #sequence_revision 10-Nov-1995 #text_change 08-Sep-2002
Cjacession: S32357
R;Marchionni, M.A; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; Henc
les, I.; Davis, J.B.; Hsuan, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M.I
Nature 362, 312-318, 1993
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A;Title: Sensory and motor neuron-derived factor. A novel heregulin variant highly expre: A;Reference number: A56943; MUID:95301541; PMID:7782315
A;Accession: A56943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q07112; GB:L12259; NID:9289413; PIDN:AAA30540.1; PID:9289414 C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
F;182-221/Domain: EGF homology <EGF>
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                                                                                                                                                                                                                                                                                                                                                                                                                            Cjaccession: 832259
R;Marchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; He. Rarchionni, M.A.; Goodearl, A.D.J.; Chen, M.S.; Bermingham-McDonogh, O.; Kirk, C.; He. Jes, I.; Davis, J.B.; Haun, J.J.; Totty, N.F.; Otsu, M.; McBurney, R.N.; Waterfield, M. Nature 362, 312-318, 1993
A;Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in the A;Title: Glial growth factors are premarively spliced erbB2 ligands expressed in the A;Status: preliminary
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                      glial growth factor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                   1;
         Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241;
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                                                                                                                                                                   1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQFL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 104.5; DB 2; Length
; Pred. No. 0.00011;
14; Mismatches 18; Indels
                                                                   Indels
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                                                                   18;
         DB 2;
   37.7%; Score 104.5; DB 2
31.2%; Pred. No. 0.00011;
ive 14; Mismatches 18
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Best Local Similarity 31.2*
Matches 15, Conservative
                                                                   15; Conservative
   Query Match
Best Local Similarity
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Best Local Similarity
Matches 15; Conserv
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R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.; Mol. Cell. Biol. 14, 1909-1319, 1994
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa A;Reference number: A56210; MUID:94158863; PMID:7509448
A;Accession: 138408
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      neu differentiation factor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 08-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Meregulin precursor, splice form beta-3 - human
NyAlternate names: glial growth factor HRG-beta-3; neuregulin
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: D4377; S32358
R;Holmes, W.B.; Silwowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park,
Science 256, 1205-1210, 1992
A;Title: Identification of heregulin, a specific activator of p185(erbB2).
A;Reference_number: A43273; MUID:92271253; PMID:1350381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U02330; NID:g408410; PIDN:AAA19955.1; PID:g408411 C;Superfamily: human heregulin; EGF homology; immunoglobulin homology F;116-155/Domain: EGF homology <EGF>
                                                                                                                                                                                            Gaps
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A;Residues: 1-6;7-16;17-30;31-38;39-58;59-92;93-120;121-125 <HAR>
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
C;Keywords: proto-oncogene
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A;Map position: 8p22-8p11
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
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                                                                                                                                                                                                                                                                                75 HLVKCAEKEKTFCVNGGECFMVKDLSNPSRYLCKCQPQFTGARCTE 120
                                                                                                                                                                                                                                                1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKH-CRCKEGYQGVRCDQ 45
                                                                                                                      38.1%; Score 105.5; DB 2; llarity 32.6%; Pred. No. 4.8e-05; Conservative 14; Mismatches 16;
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F;182-221/Domain: EGF homology <EGF>
                                                                                         Query Match
Best Local Similarity
Laber 15, Conserve
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Best Local Similarity
Thes 15; Conserva
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A; Residues: 1-175 < RES>
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neu differentiation factor - rat
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Best Local Similarity
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15; Conserv
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Signed 256, 1206-1210, 1992
A;Title: Identification of heregulin, a specific activator of p185 (erbB2).
A;Reference number: A43273; MUID:92271253; PMID:1350381
A;Reference number: A43273; MUID:92271253; PMID:1350381
A;Reference number: A43273; MUID:92271253; PMID:1350381
A;Residues: 1-637 - HOLD
A;Reference number: A6210; MUID:9415863; PMID:7509448
A;Residues: 1-637 - HOLD
A;Residues: 119-406 - RRES
A;Residues: 119
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C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: B43273;Mulb. 31-Dec-1993 #text_change 09-Jul-2004
R;Holmes, W.E.; Sliwkowski, M.X.; Akita, R.W.; Henzel, W.J.; Lee, J.; Park, J.W.; Yansux
Science 256, 1205-1210, 1992
A;Title: Identification of heregulin, a specific activator of p185(erbB2).
A;Reference number: A43273; MulD:92271253; PMID:350381
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A;Title: Glial growth factors are alternatively spliced erbB2 ligands expressed in t A;Reference number: S32357; MUID:93205115; PMID:8096067
A;Accession: 323257; MUID:93205115; PMID:8096067
A;Actatus: preliminary
A;Molecule type: mRNA
A;Residues: 1-422 cMRNA
A;Residues: 1-422 cMRNA
A;Gsuesreferences: GB:L12260; NID:922047; PIDN:AAB59622.1; PID:9292048
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
F;363-402/Domain: EGF homology <EGF>
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31.2%; Pred. No. 0.00025;
tive 14; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 37.7%; Score 104.5; DB 2; Best Local Similarity 31.2%; Pred. No. 0.00018; Matches 15; Conservative 14; Mismatches 18;
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A;Cross-references: UNIPROT:002297

R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.;

Mol. Cell. Biol. 14, 1909-1919, 1994

A;Title: Structural and functional aspects of the multiplicity of Neu differentiation fa
A;Reference number: A56210; MUID:94158863; PMID:7509448

A;Reference number: A56210; MUID:94158863; PMID:7509448

A;Reference number: A56210; MUID:94158863; PMID:7509448

A;Reference number: A56210; MUID:9416863; PMID:7509448

A;Reference number: A56210; MID:940865; PIDN:AAA19953.1; PID:9408407

C;Genetics: A7,95-418, Yr

C;Genetics: A7,95-418, Yr
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R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.
R;Wen, D.; Suggs, S.V.; Karunagaran, D.; Liu, N.; Cupples, R.L.; Luo, Y.; Janssen, A.M.
A;Title: Structural and functional aspects of the multiplicity of Neu differentiation for A;Reference number: A56210; MUID:94188863; PMID:7509448
A;Accession: A56210
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C;Date: 29-May-1998 #sequence revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: 161718; 16171; 1712; 1712; 1712; 1712; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713; 1713
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-636 cRES;
A;Accession: 161721
A;Accession: 161721
A;Accession: 161721
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Accession: 1-444, A', 446-636 cRE2>
A;Cross-references: EMBL:U02321; NID:g408392; PIDN:AAA19946.1; PID:g408393
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 08-Sep-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: EMBL:U02315; NID:9408380; PIDN:AAA19940.1; PID:9408381
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Gene: GDB:HGL
A;Cross-references: GDB:132656; OMIM:142445
A;Map position: 8p22-8p11
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47
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larity 31.2%; Pred. No. 0.00025;
Conservative 14; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: alternative splicing F;182-221/Domain: EGF homology <EGF>
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A;Accession: 161720
A;Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A;Residues: 1-298,386,'V',388,'TR',391 <RE3>
A;Residues: 1-298,386,'V',388,'TR',391 (RE3>
C;Superferences: EMBL:U02322; NID:g408390; PIDN:AAA19945.1; PID:g408391
C;Superfamily: human heregulin; EGF homology; immunoglobulin homology
F;182-221/Domain: EGF homology <EGF>

Gaps Query Match 37.0%; Score 102.5; DB 2; Length 636; Best Local Similarity 31.2%; Pred. No. 0.00042; Matches 15; Conservative 13; Mismatches 19; Indels 1;

1;

à q Search completed: November 2, 2004, 13:28:22 Job time : 39 secs

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2, 2004, 13:27:45; Search time 128 Seconds (without alignments) 119.048 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL 47
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| Cgn2_6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US07 WWW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06 WWW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08 WWW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08 WWW PUB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/1/pubpaa/US00B_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1370721 seqs, 324215800 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                         OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                        November
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	US-09-817-647-4	US-09-817-647-8	US-09-877-665-4	US-09-877-665-8	US-10-136-573A-4	US-10-136-573A-8	US-10-215-862-4	US-10-215-862-8	US-10-240-411-6	118-10-609-370-2	TIS-09-817-647-7	113-09-877-665-7	US-10-136-573A-7	
	DB	١٥	σ	σ	σ	13	13	14	14	16	15	σ	σ	13	
	Query Match Length DB	47	47	47	47	47	47	47	47	48	157	360	360	360	
æ	Query	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	
	Score	277	277	277	277	277	277	277	277	277	277	277	277	277	
	Result No.	Н	6	m	4	'n	9	7	80	σ	10	11	12	13	

233,,,	Sequence 23, Appl Sequence 23, Appl Sequence 23, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli	00441111	Sequence 12, Appl1 Sequence 12, Appl Sequence 35, Appl Sequence 35, Appl Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl
360 14 US-10-215-862-7 362 9 US-09-817-647-3 362 9 US-09-877-665-3 362 13 US-10-115-573A-3 362 14 US-10-215-862-3 696 9 US-09-817-647-23	13 US-10-136-573A 14 US-10-136-862-9 9 US-09-817-641-2 9 US-09-877-665-2 13 US-10-136-573A 14 US-10-136-862-9 9 US-09-817-641-6 9 US-09-817-665-6 13 US-10-136-5573A	0108111	14 US-10-022-609- 14 US-10-022-609- 9 US-09-795-668-3 9 US-09-946-807-3 9 US-09-795-668-3 9 US-09-795-668-3 9 US-09-795-686-3 9 US-09-946-807-3
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ALIGNMENTS

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APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/817,647 FILING DATE: 26-Mar-2001 CLASSIFCATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ 1D NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/107,979
FILING DATE: <UNKnown>
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                            Sequence 4, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
                                                                                                                                                                                              NUMBER OF SEQUENCES:
RESULT 1
US-09-817-647-4
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US-09-877-665-4
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US-09-877-665-4
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Sequence 8, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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100.0%; Score 277; DB 9; Length 47;

Best Local Similarity 100.0%; Pred. No. 4.3e-26;

Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                               1 HEKRCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                                                                                                                                                                                Length 47;
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                                                                                                NRG3 EGF-like domain/amino acid seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION TOTALS

COMPUTER: 15.5 inch, 1.44 Mb floppy disk COMPUTER: 15M PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Windatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/817,647

FILING DATE: 26-Mar-2001

CLASSIFICATION: «Unknown.)

PRIOR APPLICATION DATA:
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1 Similarity 100.0%; Score 277; DB 9;
47; Conservative 0; Mismatches 0:
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ATPLICATION NUMBER: 09/107,979
FILING DATE: CUNKNOWN:
ATTORNEY AGENT INFORMATION:
NAME: COLLEY, Deirdre L.
REGISTRATION NUMBER: 36,487
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                             OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 47 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
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                           LENGTH: 47 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  650/952-9881
                                                                                                                                       LOCATION: 1-47
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 650/952-988
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 23
                                                                        TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
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                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
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                                                                                                FEATURE
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APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
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TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
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47
                             1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPASSIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 277; DB 9;
100.0%; Pred. No. 4.3e-26;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION SOURCE.

APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-Jun-1998
ATTORNEY, AGENT INFORMATION-1998
ATTORNEY, AGENT INFORMATION-
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET WUMBER: P1084R1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/255-2066
TELEFAX: 650/352-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Jun-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                    STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09877665 Patent No. US20020164680A1 GENERAL INFORMATION:
                                                                                                                                                                    ; sequence 4, Application US/09877665; Patent No. US20020164680A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 1-47
IDENTIFICATION METHOD:
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LENGTH: 47 amino ac
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                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 47; Conserva
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US-09-877-665-8
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Sequence 8, Application US/10136573A

Publication No. US20020161200A1

SEQUENCE B. Application US/10136573A

Publication No. US20020161200A1

SEQUENCE B. Application No. US20020161200A1

SEDENCE B. INFORMATION:

APPLICANT: Canag. Paul J.

APPLICANT: Chang, Dong Xiao

TITLE OF INVENTION: Uses Therefor

TITLE OF INVENTION: Uses Therefor

TITLE OF INVENTION: Uses Therefor

CURRENT APPLICATION NUMBER: US/10/136,573A

CURRENT APPLICATION NUMBER: US 09/480,977

PRIOR APPLICATION NUMBER: US 08/480,977

PRIOR APPLICATION NUMBER: US 08/480,437

PRIOR PILING DATE: 1997-07-24

SEQUENCE SEQUENCE: 1997-07-09

NUMBER OF SEQUENCE: 23

TENNER APPLICATION NUMBER: US 60/052,019

SEQUENCE SEQUENCE: 23

TENNER APPLICATION NUMBER: US 60/052,019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-215-862-4

10-216-215-862-4

1 Sequence 4, Application US/10215862

1 Publication No. US20030056166A1

1 GENERAL INFORMATION:
1 APPLICANT: Godowski, Paul J.
1 APPLICANT: Ark, Melanie Rose
1 APPLICANT: Arbang, Dong Xiao
1 TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and
1 TITLE OF INVENTION: Uses Therefor
1 TITLE OF INVENTION: Uses Therefor
1 TITLE OF INVENTION: Uses 1004R1D2C1
1 CURRENT PAPLICATION NUMBER: US 09/126,663
1 FRIOR APPLICATION NUMBER: US 09/126,663
1 PRIOR APPLICATION NUMBER: US 08/899,437
1 PRIOR PILING DATE: 1997-07-24
1 PRIOR FILING DATE: 1997-07-09
1 NUMBER OF SEQ ID NOS: 23
2 SEQ ID NOS: 23
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                                                   Gaps
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                                                                                                                                 1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
                                                 Indels
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100.0%; Pred. No. 4.3e-26;
tive 0; Mismatches 0;
                    Pred. No. 4.3e-26;
Mismatches 0;
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100.0%; Pred. No. 4.3e-26;
tive 0; Mismatches 0;
            Best Local Similarity 100.0%; P:
Matches 47; Conservative 0;
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 47; Conserva
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Sequence 4, Application US/10136573A

Publication No US20020161200A1

GENERAL INFORMATION:

APPLICANT: Mark, Melanie Rose

APPLICANT: Calang, Dong Xiao

TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and

TITLE OF INVENTION: Uses Therefor

TITLE OF INVENTION: Uses Therefor

TITLE OF INVENTION: Uses Therefor

CURRENT APPLICATION NUMBER: US/10/136,573A

CURRENT RILING DATE: 2000-01-11

PRIOR FILING DATE: 2000-01-11

PRIOR FILING DATE: 1997-07-24

PRIOR FILING DATE: 1997-07-24

PRIOR FILING DATE: 1997-07-09

NUMBER OF SEQ ID NOS: 23

UNUMBER OF SEQ ID NOS: 23

CREMENT HON SAPILATION NUMBER: US 60/052,019

PRIOR FILING DATE: 1997-07-09

TYPE: PRIOR FILING DATE: 1997-07-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: NRG3 EGF-like domain/amino acid seq.
                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WithDatin (Genentech) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/877,665 FILING DATE: 08-Jun-2001 CLASSIFICATION APPLICATION NUMBER: US/09/109,206 FILING DATE: 30-Jun-1998 ATTORNEY/AGENT INFORMATION:

NAME: COALEY, DEICATE 1. REGISTRATION NUMBER: 36,487 REFERENCE/DOCKET NUMBER: 36,487 REFERENCE/DOCKET NUMBER: 91084R1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGIH: 47 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: Amino Acid
TOPOLOGY: Linear
                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
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US-09-877-665-8

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US-10-136-573A-4

Query Match

g ð

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Sequence 7, Application US/09817647;
Sequence 7, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 HFKPCRDKDLAYCLNDGBCFVIETLTGSHKHCRCKEGYQGVRCDQFL 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winbatin (Genentech) CURRENT APPLICATION NUMBER: US/09/817,647 FILING DATE: 26-Mar-2001 CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/107,979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 277; DB 15; Best Local Similarity 100.0%; Pred. No. 1.4e-25; Matches 47; Conservative 0; Mismatches 0;
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NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE, DOCKET WMBER: P1084R1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
                                                                     TITLE OF INVENTION: Heregulin-Like Factor FILE REPERENCE: P7383D1
CURRENT APPLICATION NUMBER: US/10/609,370
CURRENT FILING DATE: 2003-07-01
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco STATE: California
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LENGTH: 360 amino acids
Sequence 2, Application US/10609370 Publication No. US20040048295A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1-360
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Homo sapiens US-10-609-370-2
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                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 2
LENGTH: 157
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APPLICANT: Harari, Daniel
APPLICANT: Harari, Daniel
APPLICANT: Yarden, Yosef
TITLE OF INVENTION: SEQUENCES ENCODING SAME AND USES THEREOF
TITLE OF INVENTION: SEQUENCES ENCODING SAME AND USES THEREOF
FILE REPERRINCE: 01/21918
CURRENT FILING DATE: 2003-05-16
PRIOR PELING DATE: 2000-04-21
NUMBER OF SEQ ID NOS: 20
SEQ TRANKE: PatentIn version 3.0
SEQ ID NO 6
LINDRING BA
                                                                                                                                                                      yequence 8, Application US/10215862
yequence 8, Application US/10215862
yeublication No. US20030036166A1
general information.
yeublication No. US20030036166A1
general information.
yepticant: Gedowski, Paul J.
yepticant: Applicant Rose
yepticant: Applicant Rose
yepticant: Zhang, Dong Xiao
yepticant: Zhang, Dong Xiao
yepticant: Plus Receptor-Specific Neuregulin Related Ligands and
yepticant in Number: US/10/215,862
yence Tiller Date: 1998-07-30
yence Reling Date: 1998-07-30
yence Reling Date: 1997-07-24
yence Reling Date: 1997-07-24
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                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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                    1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
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100.0%; Pred. No. 4.3e-26;
ative 0; Mismatches 0;
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Sequence 6, Application US/10240411
Publication No. US20040121326A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
US-10-215-862-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Mus musculus US-10-240-411-6
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Best Local Similarity
Matches 47; Conserv
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US-10-609-370-2
                                                                                                                                                  RESULT 8
US-10-215-862-8
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LENGTH: 47
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TYPE: PRT

RESULT 9

ð g TYPE: PRT

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APPLICANT: Godowski, Paul J.
APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie Rose
APPLICANT: Mark, Melanie Rose
APPLICANT: Lang, Dong Xiao
ITILE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and
ITILE OF INVENTION: Uses Therefor
FILE REPERENCE: P1084RL02
CURRENT PELLING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US 09/480,977
PRIOR APPLICATION NUMBER: US 09/480,977
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09817647; Patent No. US20020082229A1; Patent No. US20020082229A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 277; DB 13;
100.0%; Pred. No. 3.3e-25;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 277; DB 14; Best Local Similarity 100.0%; Pred. No. 3.3e-25; Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/10215862
Publication No. US20030036166Al
GENERAL INFORMATION:
                   US20020161200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0°
Best Local Similarity 100.0°
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 360
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US-10-215-862-7
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US-09-817-647-3
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TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                     Gaps
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100.0%; Score 277; DB 9; Length 360;
Best Local Similarity 100.0%; Pred. No. 3.3e-25;
Matches 47; Conservative 0; Mismatches 0; Indels
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                                                                                                                                 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 18M PC compatible OPERATING SYSTEM: PC-DOS/MS-DS SOFTWARE: WinPatin (Genentech) CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/877,665 FILING DATE: 08-Jun-2001 CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION: <UNKNOWN>
PRIOR APPLICATION: <UNKNOWN>
                                                                                 Query Match
100.0%; Score 277; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.38-25;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-Jun-1998
ATTORNEY/AGENT INFORMATION:
NAME: COTLEY, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET UNBER: P1084R1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1-360
IDENTIFICATION METHOD:
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-10-136-573A-7
; Sequence 7, Application US/10136573A
                                                                                                                                                                                                                                                                                                              Sequence 7, Application US/09877665
Patent No. US20020164680A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 360 amino acids
TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
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                                US-09-817-647-7
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US-09-877-665-7
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Search completed: November 2, 2004, 13:39:26 Job time : 129 secs

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Sequence 4, Appli
Sequence 8, Appli
Sequence 4, Appli
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                                                                                          November 2, 2004, 13:45:37; Search time 127 Seconds (without alignments) 119:985 Million cell updates/sec
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Sequence 4, Appli
Sequence 8, Appli
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Sequence 8,
Sequence 6,
Sequence 2,
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Sequence 8,
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Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/USO6_PUBCOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
Cgn2_6/ptodata/1/pubpaa/DEWGOMB.pep:*
Cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-877-665-8
US-10-136-573A-4
US-10-136-573A-8
US-10-136-573A-8
US-10-215-862-8
US-10-240-411-6
US-10-609-370-2
US-09-877-665-7
US-09-877-665-7
US-10-136-573A-7
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                                                                                                                                                                                                                                                                                     1370721 seqs, 324215800 residues
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US-09-817-647-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications AA:
                                                              OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Sequence 7, Appli Sequence 3, Appli Sequence 3, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 19, Appli Sequence 210620, Sequence 210620, Sequence 210620, Sequence 210620, Sequence 211339, Sequence 211339, Sequence 211339, Sequence 211339,	equence 62587, equence 47208, equence 106, Api
US-10-215-862-7 US-09-817-647-3 US-09-817-665-3 US-10-136-573A-3 US-10-215-862-3 US-09-817-665-23 US-09-817-665-23 US-09-817-665-23 US-09-817-665-2 US-10-136-573A-2 US-10-136-573A-2 US-10-136-573A-2 US-10-136-573A-2 US-10-136-573A-2 US-10-136-573A-2 US-10-136-573A-1 US-09-817-665-6 US-10-136-573A-1 US-09-817-665-6 US-10-136-573A-1 US-09-817-665-1 US-10-136-573A-1 US-09-817-665-1 US-10-136-573A-1	-10-425-114-62 -10-425-114-47 -10-236-392-10
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US-09-817-647-4

Sequence 4, Application US/09817647

Sequence 4, Application US/09817647

Patent No. US2020229A1

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao

TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related

Idands and Uses Therefor

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

STREET: 1 DNA Way

CITY: South San Francisco

STATE: Callifornia

COUNTRY: USA

ALIGNMENTS

ZIP: 94080

COMPUTER READABLE FORM:

WEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOSTWARE: Windatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/817,647
FILING DATE: 26-Mar-2001

PRIOR APPLICATION: CURKNOWN:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 09/107,979
FILING DATE: CURKNOWN:

ATTORNEY/AGENT INFORMATION:
NAME: CONDEY, Delirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/25-2066
TELEPHONE: 650/25-2066
TELEPHONE: 650/25-2066
TELEPHONE: 650/25-2066

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HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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Best Local Similarity
Matches 47; Conserva
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US-09-877-665-8
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                                                                                                                RESULT 3
US-09-877-665-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                  Length 47;
                                                                                                                                                                                                                                                                                                                                                1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
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                                                                                                             NRG3 EGF-like domain/amino acid seq. 1-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC COMPATIBLE COMPATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/817,647
FILING DATE: 26-Mar-2001
CLASSIFICATION: CURNOWN>
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 09/107,979
FILING DATE: CURIONNI
ATTORNEY, AGENT INFORMATION:
NAME: Conley, Deirdre L.
REGISTRATION NUMBER: 36.487
REFERENCE/DOCKET NUMBER: 91084R1-2
TELECOMUNICATION:
TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                     LOCATION: 1-47
IDENTIFICATION METHOD:
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSE: Genettech, Inc.
STREET: I DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD: OTHER INFORMATION:
                                      LENGTH: 47 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
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                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
                                                                                 TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
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                                                                                                                          NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE
                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-817-647-8
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US-09-817-647-8
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Sequence No. US20020164680A1
GENERAL INFORMATION:
APPLICANN: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor
                                                                                                                                                                                                                  APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related Ligands and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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1 HFKPCRDKDLAYCLNDGBCGFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 47; DB 9; Length 47; 100.0%; Pred. No. 1.5e-43; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: NRG3 EGF-like domain/amino acid seq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIF: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Uun-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-Uun-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: COLLEY, DEITGRE L.
REGISTRATION NUMBER: 36,487
REFERENCE, DOCKET NUMBER: PI084RI-1
TELECOMMINICATION INFORMATION:
TELEPHONE: 650/225-2066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
CORRESPONDENCE Geneticech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                Sequence 4, Application US/09877665 Patent No. US20020164680A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 1-47
IDENTIFICATION METHOD:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 47 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 4
                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47; Conservative
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APPLICANT: Godowski, Paul J.
APPLICANT: Mark, Melanie Rose
APPLICANT: Mark, Melanie Rose
FULL APPLICANT: Chang, Dong Xiao
ITILE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and
TITLE OF INVENTION: Uses Therefor
FULE REFERENCE: P1084ALCZ
CURRENT APPLICATION NUMBER: US/10/136,573A
CURRENT FILING DATE: 2002-04-29
PRIOR PILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: US 09/480,977
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
PRIOR FILING DATE: 1997-07-24
MUMBER OF SEQ ID NOS: 23
SEQ ID NOS: 23
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Publication No. US20030036166A1
GENURAL INFORMATION:
GENURAL INFORMATION:
APPLICANT: Godowski, Paul J.
TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and TITLE OF INVENTION: Uses Therefor FILE REFERENCE: P1084R1D2C1
CURRENT APPLICATION NUMBER: US/10/215,862
CURRENT APPLICATION NUMBER: US 09/126,663
FRIOR APPLICATION NUMBER: US 09/126,663
FRIOR APPLICATION NUMBER: US 08/899,437
FRIOR FILING DATE: 1997-07-24
FRIOR FILING DATE: 1997-07-09
                                                Gaps
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Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 47; Conservative 0; Mismatches 0; Indels
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                                                                                          1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
                                          Indels
                   red. No. 1.5e-43;
Mismatches 0;
                Pred. No.
                                                                                                                                                                                                                                                                                  Sequence 8, Application US/10136573A Publication No. US20020161200A1 GENERAL INFORMATION:
              ilarity 100.0%; P:
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
           Best Local Similarity Matches 47; Conserv
                                                                                                                                                                                                                                                           US-10-136-573A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Sequence 4, Application US/10136573A

Publication No. US20020161200A1

GENERAL INFORMATION:

APPLICANT: Godowski, Paul J.

APPLICANT: Mark, Melanie Rose

APPLICANT: Mark, Melanie Rose

APPLICANT: Zhang, Dong Xiao

TITLE OF INVENTION: Uses Therefor

TITLE OF INVENTION: Uses Therefor

FILE REPERENCE: P1084R122

CURRENT APPLICATION NUMBER: US/10/136,573A

CURRENT APPLICATION NUMBER: US 09/480,977

PRIOR APPLICATION NUMBER: US 08/999,437

PRIOR APPLICATION NUMBER: US 08/999,437

PRIOR FILING DATE: 1997-07-24

PRIOR FILING DATE: 1997-07-24

PRIOR FILING DATE: 1997-07-09

NUMBER OF SEQ ID NOS: 23

LENGTH: 47
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Query Match

Best Local Similarity 100.0%; Pred. No. 1.5e-43;

Matches 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: NRG3 EGF-like domain/amino acid seg.
                                                                                                                                                   MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Jun-2001
CLASSIFICATION: <UNKNOWN.
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-4un-1998
ATTORNEY/ABENT INFORMATION:
NAME: CONley, Deirdre L.
RECISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: 91084R1-1
TELECOMMUNICATION INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) CTHER INFORMATION: SEQUENCE DESCRIPTION: SEQ ID NO: 8: US-09-877-665-8
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 47 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
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                                                                               COUNTRY:
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FEATURE

US-10-136-573A-4

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Gaps

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100.0%; Score 47; DB 14; Length 47; 100.0%; Pred. No. 1.5e-43; ive 0; Mismatches 0; Indels

Conservative

Query Match Best Local Similarity Matches 47; Conserv

Length 47;

DB 13;

100.0%; Score 47;

CRGANISM: Homo sapiens US-10-136-573A-4

Query Match

TYPE: PRT

; ORGANISM: Homo sapiens US-10-215-862-4

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Sequence 7, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 HFKPCRDKDLÁYCLNDGECFVIETLTGSHKHCRCKEGYÓGVRCDÓFL 77
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
CCMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
100.0%; Score 47; DB 15;
Best Local Similarity 100.0%; Pred. No. 4.4e-43;
Matches 47; Conservative 0; Mismatches 0;
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RILING DATE: <UNKNOWN>
NAME: CONLEY, Deirdre L.
REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GORRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/817,647
FILING DATE: 26-Mar-2001
CLASSIFICATION: «Unknown»
                                                                                                     TITLE OF INVENTION: Heregulin-Like Factor TITLE OF INVENTION: Heregulin-Like Factor FILE REFERENCE: PF383D1
CURRENT PEPLICATION NUMBER: US/10/609,370
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: 09/097,681
PRIOR FILING DATE: 1998-06-16
PRIOR FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 22
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 360 amino acids TYPE: Amino Acid
Sequence 2, Application US/10609370 Publication No. US20040048295A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1-360 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 157
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US-09-817-647-7
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US-10-240-411-6

i Sequence 6, Application US/10240411

; Publication No. US20040121326A1

; Publication No. US20040121326A1

; Publication No. US20040121326A1

; APPLICANT: Harari, Daniel

; APPLICANT: Harari, Daniel

; TITLE OF INVENTION: NOVEL GROWTH FACTOR WHICH ACTS THROUGH ERB B-4 RECEPTOR TYROSINE

; TITLE OF INVENTION: SEQUENCES ENCODING SAME AND USES THEREOF

; TITLE OF INVENTION: SOU3-05-16

; PRIOR APPLICATION NUMBER: US 09/553,769

; PRIOR APPLICATION NUMBER: US 09/553,769

; PRIOR PILING DATE: 2000-04-21

; NUMBER OF SEQ ID NOS: 20

; SEQ ID NOS: 20

; SEQ ID NO 6

; TENCHUL OF T
                                                                                                                                                                                                                          Sequence 8, Application US/10215862
; Sequence 8, Application US/10215862
; Publication No. US20030036166A1
; GENERAL INFORMATION:
; APPLICANT: Godowski, Paul J.
; APPLICANT: Anang, Dong Xiao
; TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and
; TITLE OF INVENTION: ExbB Receptor-Specific Neuregulin Related Ligands and
; FILE REFERENCE: P1084R1D2C1
; CURRENT APPLICATION NUMBER: US/10/215,862
; CURRENT APPLICATION NUMBER: US/0/20-2-4
; PRIOR FILING DATE: 1998-07-30
; PRIOR FILING DATE: 1997-07-24
; PRIOR FILING DATE: 1997-07-24
; PRIOR FILING DATE: 1997-07-09
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 8
; LENGTH: 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 100.0%; Score 47; DB 14; Length 47; Similarity 100.0%; Pred. No. 1.5e-43; 47; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 HFKPCRDKDLAYCLNDGECFVIETLIGSHKHCRCKEGYQGVRCDQFL 47
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                                                             1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                     HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
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100.0%; Score 47; DB 16;
Best Local Similarity 100.0%; Pred. No. 1.6e-43;
Matches 47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
US-10-609-370-2
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US-10-215-862-8
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RESULT 12

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JOHNEAL ALLYCHAIL AND AND AND AND AND APPLICANT: Mark, Melanie Rose

JAPPLICANT: Mark, Melanie Rose

JAPPLICANT: Mark, Melanie Rose

JAPLICANT: Mark, Melanie Rose

JAPLICANT: Margin Ming Xiao

JAPLICANT: Margin Ming Xiao

JAPLICANT: Margin Ming Receptor-Specific Neuregulin Related Ligands and TITLE OF INVENTION: Uses Therefor

JAPLICANT: Margin Ming Receptor-Specific Neuregulin Related Ligands and TITLE OF INVENTION: Uses Therefor

JAPLICANTON: Uses Therefor

JAPLICANTON NUMBER: US 09/480, 977

PRIOR PILING DATE: 1297-07-24

PRIOR FILING DATE: 1997-07-24

PRIOR FILING DATE: 1997-07-09

JAPLICANTON NUMBER: US 60/052, 019

PRIOR FILING DATE: 1997-07-09

JAPLICANTON NOWER: US 60/052, 019

JAPLICANTON NOWER: US 60/052, 019

JAPLICANTON NOWER: US 60/052, 019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10215862
Publication No. US20030036166A1
GENERAL INFORMATION:
APPLICANT: Godowski, Paul J.
APPLICANT: AAPLICANT: AAR, Melanie Rose
APPLICANT: AAPLICANT: AAR, Melanie Rose
APPLICANT: AARD Becceptor-Specific Neuregulin Related Ligands and
TITLE OF INVENTION: ExbB Receptor-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 13; Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 HFRPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332
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100.0%; Score 47; DB 14; Length 360;
Best Local Similarity 100.0%; Pred. No. 9e-43;
Matches 47; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TILE REFERENCE: P1084R1D2C1
CURRENT APPLICATION NUMBER: US/10/215,862
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 09/126,663
PRIOR PILING DATE: 1998-07-30
PRIOR PLILNG DATE: 1997-07-24
PRIOR APPLICATION NUMBER: US 08/899,437
PRIOR PLILNG DATE: 1997-07-09
PRIOR APPLICATION NUMBER: US 60/052,019
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09817647
Patent No. US20020082229A1
GENERAL INFORMATION:
                US20020161200A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 47; Conserv
                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-136-573A-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Godowski, Paul J., Mark, Melanie Rose, Zhang, Dong Xiao
TITLE OF INVENTION: ErbB Receptor-Specific Neuregulin Related
Ligands and Uses Therefor
                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                            Length 360;
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                                                                                                                                                               0; Indels
                                                                                                                                                                                                           1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL
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hea 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk COMPUTER: 1BM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                 Query Match
100.0%; Score 47; DB 9;
Best Local Similarity 100.0%; Pred. No. 9e-43;
Matches 47; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Conley, Deirdre L. REGISTRATION NUMBER: 36,487
REFERENCE/DOCKET NUMBER: P1084R1-1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/877,665
FILING DATE: 08-Jun-2001
CLASSIFICATION: <URKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/109,206
FILING DATE: 30-Jun-1998
ATTORNEY/AGENT INFORMATION:
OTHER INFORMATION:
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/09877665
Patent No. US20020164680Al
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/10136573A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 650/225-2066
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 360 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-136-573A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE
                                                US-09-817-647-7
                                                                                                                                                                                                                                                                                                                                                                US-09-877-665-7
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Gaps

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47

RESULT 13

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TITLE OF INVENTION: ExbB Receptor-Specific Newregulin Related
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: Geneatech, Inc.
STREET: 1 by 4000
COMPINEY: South Na Way
CITY: South Na Way
CITY: South San Francisco
STRATE: Callfornia
COUNTRY: USA
COUNTRY: CALLON DATA:
CASSIFICATION NAME: USA)09/617,647
FILLING DATE: USA
COUNTRY: OSA
COUNTRY: OSA
COUNTRY: OSA
COUNTRY: OSA
COUNTRY: USA
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Search completed: November 2, 2004, 13:57:13 Job time: 127 secs

288 HFKPCKDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 334

1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 2, 2004, 13:37:06 ; Search time 38 Seconds (without alignments) 119:005 Million cell updates/sec

1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL 47 US-09-107-979-4 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

283416 seqs, 96216763 residues Searched:

0 Word size :

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	T44447	RSMXS	S59948	856660	H86252	S56661	S38370	T19545	MMFFB1	JC2568	B48083	F69592	A44462	\$33623	G71312	AE1637	F72220	H69459	H83970	T06326	G98308	AD2974	G75436	J01395	A64069	T48057	T52077	A89890	10
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Query Match 14.9%; Score 7; DB 1; Best Local Similarity 100.0%; Pred. No. 3.9; Matches 7; Conservative 0; Mismatches

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9	9	9	9	9	9	9	9	9	9	9	9	9	9	9	9
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Cidate: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004 Richard, D.; Sliwkowski, M.X.; Mark, M.; Frantz, G.; Akita, R.; Sun, Y.; Hillan, K.; Crox Richang, D.; Sliwkowski, M.X.; Mark, M.; Frantz, G.; Akita, R.; Sun, Y.; Hillan, K.; Crox Proc. Natl. Acad. Sci. U.S.A. 94, 9562-9567, 1997 A;Title: Neuregulin-3 (NRG3): A novel neural tissue-enriched protein that binds and activ A;Reference number: Z22773; MUID:97420720; PMID:9275162 A;Accession: T44447 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Accession: T4447 A;Status: preliminary A;Accession: T4447 A;Cross-references: UNIPROT:035181; EMBL:AF010130; NID:g2429163; PIDN:AAB70914.1; PID:g24;Genetics: A;Genetics: A;Genetics: C;Superfamily: mouse neuregulin-3
<pre>Query Match</pre>
RESULT 2 R5MX5 ribosomal protein L5 - Methanococcus vannielii c;bosomal mar.1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004 C;Accession: S05617 #seck, A. J. Mol. Biol. 2099, 21-36, 1989 A;Title: Organization and structure of the Methanococcus transcriptional unit homologous s ribosomes S ribosomes A;Reference number: S05611; MUID:90040717; PMID:2530355 A;Accession: S05617 A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: DNA A;Molecule type: UNIPROT:P14029; EMBL:X16720; NID:g44754; PIDN:CAA34693.1; PID:g44761 C;Superfamily: ribosomal protein L5/L11 C;Keywords: protein biosynthesis; ribosome

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Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C., C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, J. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-408 <STO>
A;Cross-references: UNIPROT:065396; GB:AE005172; NID:g3157944; PIDN:AAC17627.1; GSPDB:GN
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A, Accession: 556733
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iive 0; Mismatches
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100.0%; Pred. No. ...
... 0; Mismatches
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A,Residues: 31-39 «XO2»
Superfamily: aminomethyltransferase
C,Superfamily: tansferase
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C, Superfamily: aminomethyltransferase
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                                                                                                                                                                                                                                                                                       aminomethyltransferase (EC 2.1.2.10) precursor - potato
N;Alternate names: glycine cleavage system protein T; glycine decarboxylase multienzyme
N;Alternate names: glycine cleavage system protein T; glycine decarboxylase multienzyme
C;Species: Solanum tuberosum (potato)
C;Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C;Accession: S59948; S40219
R;Kopriva, S: Bauwe, H.
Plant Physiol. 104, 1079-1080, 1994
A;Title: T-protein of glycine decarboxylase from Solanum tuberosum.
A;Reference number: S59948; MUID:94218396; PMID:8165246
A;Accession: S59948
A;Accession: S59948
A;Accession: S59948
A;Residues: 1-406 «KOP>
A;Residues: 1-406 «KOP>
A;Residues: 1-406 «KOP>
A;Cobertics: UNIPROT:P54260; EMBL:Z25862; NID:g438253; PIDN:CAA81081.1; PID:g4382
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993
A;Cobertics: A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1993
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N'Alternate names: glycine cleavage system protein T
C;Species: Flaveria pringlei
C;Species: Plaveria pringlei
C;Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56660; &40217
R;Kopriva, S.; Turner, S.R.; Rawsthorne, S.; Bauwe, H.
R;Kopriva, S.; Turner, S.R.; Rawsthorne, S.; Bauwe, H.
R;Ropriva, S.; Turner, S.R.; Rawsthorne, S.; Rawsthorne, S
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A;Molecule type: mRNA
A;Residues: 1-407 <KOP>
A;Residues: 1-407 <KOP>
A;Cross-references: UNIPROT:P49363; EMBL:Z25858; NID:g438004; PIDN:CAA81077.1; PID:g4380
C;Superfamily: anihomethyltransferase
C;Keywords: transferase
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C,Superfamily: transferase
F,1-29/Domain: transit peptide (mitochondrion) #status predicted
F,30-406/Product: aminomethyltransferase #status predicted <MAT>
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100.0%; Pred. No. 7.7;
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100.0%; Pred. No. 7.7;
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Les 7; Conserv
                                                                                                39 VIETLIG 45
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Keywords: basement membrane; calcium binding; cell binding; coiled coil; extracellular: 1-26/Domain: signal sequence #status predicted <SIG>27-1799/Product: laminin beta-1 chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;51-56/Disulfide bonds: #status predicted
F;140,203,234,489,593,1053,1248,1303,1332,1343,1475,1495,1517,1583,1646,1705/Binding site
F;1191,1194,1788/Disulfide bonds: interchain #status predicted
   C;Keywords: basement membrane; calcium binding; cell binding; coiled coil; ext F;1-26/Domain: signal sequence #status predicted <SIG>F;27-288/Domain: signal sequence #status predicted <SIG>F;27-288/Domain: V < LDOMS>
F;289-561/Domain: V < LDOMS>
F;289-561/Domain: Juminin-type EGF-like homology <LEGO>F;280-354/Domain: laminin-type EGF-like homology <LEGO>F;387-417/Domain: laminin-type EGF-like homology <LEGO>F;480-477/Domain: laminin-type EGF-like homology <LEGO>F;581-561/Domain: laminin-type EGF-like homology <LEGO>F;581-561/Domain: laminin-type EGF-like homology <LEGO>F;581-561/Domain: laminin-type EGF-like homology <LEGO>F;791-886/Domain: laminin-type EGF-like homology <LEGO>F;881-882/Domain: laminin-type EGF-like homology <LEGO>F;881-882/Domain: laminin-type EGF-like homology <LEGO>F;881-993/Domain: laminin-type EGF-like homology <LEGO>F;881-993/Domain: laminin-type EGF-like homology <LEGO>F;881-993/Domain: laminin-type EGF-like homology <LEGO>F;1045-1093/Domain: laminin-type EGF-like homology <LEGO>F;1050-1093/Domain: laminin-type EGF-like homology <LEGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cispecies: Rhizobium meliloti
Cispecies: Rhizobium meliloti
Cispecies: Nacession: JC2568
Ricession: JC2568
Ricession: JC2568
Ricession: JC2568
A;Title: Rhizobium meliloti homologs of Escherichia coli mur genes.
A;Title: Rhizobium meliloti homologs of Escherichia coli mur genes.
A;Reference number: JC2567; MUID:95011665; PMID:7926844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome segregation protein CSE2 - yeast (Saccharomyces cerevisiae) NyAlternate names: protein N2046; protein YNR010w C;Species: Saccharomyces cerevisiae C;Species: Saccharomyces cerevisiae C;Species: 26-May-1994 #text_change 09-Jul-2004 C;Accession: B48083; S45132; S48347; S63336; S43944 R;Xiao, Z.; McGrew, J.T.; Schroeder, A.J.; Fitzgerald-Hayes, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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C,Superfamily: phospho-N-acetylmuramoyl-pentapeptide-transferase
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cive 0; Mismatches
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100.0%; Pred. No. 32;
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mraY protein - Rhizobium meliloti (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100...
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C; Genetics:
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Best Local Similarity
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A; Residues: 1-118 < LEA>
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B48083
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A;Cross-references: UNIPROT:P49364; EMBL:X74793; NID:9407474; PIDN:CAA52800.1; PID:94074
C;Superfamily: aminomethyltransferase
C;Keywords: transferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-1264 <MIL>
A;Cross-references: UNIPROT:Q18291; EMBL:Z73970; PIDN:CAA98243.1; GSPDB:GN00023; CESP:C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             laminin beta-1 chain precursor - fruit fly (Drosophila melanogaster)

NyAlternate names: laminin chain B1

C;Species Drosophila melanogaster

C;Date: 30-Unn-1991 #sequence revision 30-Unn-1991 #text_change 09-Jul-2004

C;Accession: A28783; S14462; B28783

R;Montell, D.J.; Goodman, C.S.

Cell 53, 463-473, 1988

A;Title: Drosophila substrate adhesion molecule: sequence of laminin B1 chain reveals dc

A;Reference number: A28783; MUID:88210471; PMID:3365769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Introns: 40/2; 92/2; 113/3; 169/3; 203/1; 227/3; 266/1; 319/3; 437/1; 636/1; 668/3; 7d
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A;Residues: 1-1790 <MONI>
A;Residues: 1-1790 <MONI>
B;Residues: 1-1790 <MONI>
R;Montell, D.J.; Goodman, C.S.
Submitted to the EMBL Data Library, June 1988
A;Description: Drosophila substrate adhesion molecule: sequence of laminin B1 chain reve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein C29A12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T19545
                                                                                                                                                                                                            Gaps
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A;Molecule type: mRNA
A;Residues: 1-667,'L',669-725,'VT',728-947,950-1790 <MON2>
A;Cross-references: EMBL:M19525; NID:g157801; PIDN:AAA28663.1; PID:g157802
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                                                                                                                                          Length 408;
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100.0%; Pred. No. 20;
tive 0; Mismatches
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                                                                                                                                14.9%; Score 7; I
100.0%; Pred. No.
tive 0; Mismatch
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A,Gene: lamBl
A,Cross-references: FlyBase:FBgn0002527
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Best Local Similarity 100.
Matches 7; Conservative
                                                                                                Query Match
Best Local Similarity
''^a Conserva
                                                                                                                                                                                                                                                                                                                                  CRDKDLA 157
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Gaps

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Length 157; 0; Indels

DB 2;

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A, Experimental gources: UNIPROT: 007920; GB: Z99117; GB: AL009126; NID: 92634966; PIDN: CAB14613. A, Experimental gource: strain 168
R; Belitsky, B.R.; Gustafsson, M.C.U.; Sonenshein, A.L.; von Wachenfeldt, C.
J. Bacteriol. 179; 5448-5457, 1997
A, Title: An 1rp-like gene of Bacillus subtilis involved in branched-chain amino acid tra A, Reference number: Z22837; MUID: 97431495; PMID: 9287000
A, Recession: T44776
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Occession: T44776
A, Genes preliminary; translated from GB/EMBL/DDBJ
A, Gross: reference: EMBLY 11043; NID: 91926275; PIDN: CAA71939.1; PID: 91926280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       allophycocyanin alpha chain - Synechocystis sp. (strain PCC 6803)
C;Species: Synechocystis sp.
A;Variety: PCC 6803
A;Variety: PCC 6803
C;Accesion: A44462, S75012
C;Accesion: A44462, S75012
J; Biol. X.; Fraenkel, P.G.; Bogorad, L.
J; Biol. Chem. 267, 22944-22950, 1992
A;Pitle: Excitation energy transfer from phycocyanin to chlorophyll in an apcA-defective and a processions and a procession and a processions and a processions and a processions and a procession and a processions and a procession and a processi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.8%; Score 6; DB 2, 100.0%; Pred. No. 41; cive 0; Mismatches
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Best Local Similarity
Matches 6; Conserv
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-161 <SU1>
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                                           A; Residues: 1-157 < KUN>
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C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: F6959; T44776
R;Accession: F6959; T44776
R;Xunst, F.; Ogasawara, M.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; ChC
A,; Ehrlich, S.D.; Bmmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fullibert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, Koetter, P.; Koningstein, G.; Rocha, E.; Roche, B.; Rosse, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Yamanoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yasunoto, K.; Yasunoto, K.; Yasunoto, K.; Yasunoto, K.; Yasunoto, K.; Yata, K.; Yoshida, K.; A;Reference number: Aspense sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: Assession: R69580; Mullisequence not shown; translation not shown
Mol. Ceil. Biol. 13, 4691-4702, 1993

A,Title: CSE1 and CSE2, two new genes required for accurate mitotic chromosome segregati
A,Reference number: A48083; MUID:93330263; PMID:8336709
A,Accession: B48083
A,Molecule type: DNA
A,Residues: 1-149 < KIA>
A,CRS references: UNIPROT:P33308; GB:L14839; NID:g349590; PIDN:AA34532.1; PID:g349591
R,Yerhasselt, P.; Aert, R.; Voet, M.; Volckaert, G.
submitted to the EMBL Data Library, January 1994
A,Description: Twelve open reading frames revealed on the 23.6 kbp segment flanking the
A,Reference number: S45119
A,Accession: S4132
A,Molecule type: DNA
A,References: EMBL:X77395; NID:g496717; PIDN:CAA54578.1; PID:g496726
A,CROS-references: EMBL:X77395; NID:g496717; PIDN:CAA54578.1; PID:g496726
A,CROS-reference number: S483347
A,Status: nucleic acid sequence not shown; translation not shown
A,Residues: 1-149 <-WES>
A,Accession: S48347
A,Status: nucleic acid sequence was submitted to the EMBL Data Library, January 1994
A,Reference number: S62310
A,Rocession: S63336
A,Reference number: S62310
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A,MOICCULE TYPE: DNA
A,ROSIQUES: 1-149 <AER>
A,Cross-references: EMBL:Z71625; NID:g1302485; PIDN:CAA96287.1; PID:g1302486; MIPS:YNR01
A,Experimental source: strain S288C
C,Genetics:
A,Gene: SGD:CSE2
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C;Superfamily: Saccharomyces chromosome segregation protein CSE2
C;Keywords: DNA binding; leucine zipper; nucleus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 149;
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A; Cross-references: UNIPROT: Q01951; GB:M77135; NID:g154453; PIDN:AAA27276.1; PID:g154454 A; Cross-references: UNIPROT: Q01951; GB:M77135; NID:g154453; PIDN:AAA27276.1; PID:g154454 A; Cross-references: DCC 6803
A; Note: sequence extracted from NCBI backbone (NCBIP:118109)
A; Note: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Cross-references: EMBL:D90910; GB:AB001339; NID:g1652956; PIDN:BAA17874.1; PID:g16529
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C,Genetics:
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C;Superfamily: phycocyanin
C;Keywords: chromoprotein; photosynthesis; phycocyanobilin
F;81/Binding site: phycocyanobilin (Cys) (covalent) #status predicted
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A;Accession: S75012
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-161 <KAN>
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100.0%; Pred. No. 41;
ive 0; Mismatches 0; Indels
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probable translation elongation factor P (efp) - syphilis spirochete
(Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
(Species: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
(SACCESSION: G71312
(R)FACESSION: G71312
(R)FASSER, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwinton, L.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDq Science 281, 375-388, 1998
Afille: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Residues: 1-161 <DIM>
A;Cross-references: UNIPROT:Q02923; EMBL:L02308; NID:g154449; PIDN:AAA69682.1; PID:g1544
A;Experimental source: PCC 6714
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1992
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allophycocyanin alpha chain - Synechocystis sp. (strain PCC 6714)
S.Species: Synechocystis sp.
A.Variety: PCC 6714
C.Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C.Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
C.Date: 19-Mar-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
R.DiMagno, L.; Haselkorn, R.
Plant Mol. Biol. 21, 835-845, 1993
A.Title: Isolation and characterization of the genes encoding allophycocyanin subunits A.Reference number: 833623; MUID:93222481; PMID:8467079
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C;Keywords: chromoprotein; photosynthesis; phycocyanobilin
F;81/Binding site: phycocyanobilin (Cys) (covalent) #status predicted
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A;Gene: TP0525
C;Superfamily: translation elongation factor EF-P
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GenCore version 5.1.6
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OM protein - protein search, using sw model

November Run on:

2, 2004, 13:29:11; Search time 193 Seconds (without alignments) 140:117 Million cell updates/sec

1 HFKPCRDKDLAYCLNDGECF.....SHKHCRCKEGYQGVRCDQFL 47 US-09-107-979-4 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

1825181 seqs, 575374646 residues Searched:

0 Word size :

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

UniProt 02:* Database

1: uniprot_sprot:* 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		homo	deoba	96 geobacte	۵	P14029 methanococc			anophe	mus muscul		Varrowi	σ	3 flaveria	36 flaveria	6 arabidops	4	oryza	rhizob	Ofuxi9 homo sapien		O7GWt5 giardia lâm	rhodopse	9	O8swv0 drosophila		-		~		
SUMMARIES	ID	NRG3 MOUSE	NRG3 HUMAN	Q74F <u>Y</u> 8	AAR33796	Q947L6	RL5_METVA	Q86 <u>D</u> G8	OBLNG9	9791J6	GCST MOUSE	GCST_SOLTU	Q6C340	GCST FLAAN	GCST_FLAPR	GCST_FLATR	GCST ARATH	GCST PEA	Q7XPR2	0981J4	06UXI9	AAQ88702	Q7QWT5	Q6N7N7	CAE27661	QBSWYO	Q18291	LMB1 DROME	<u>06uc</u> 08	AAR05332	080554	Q9BDC5
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Q6jgx3 uncultured	Q6jgy1 uncultured	Aas57675 unculture	Aas57683 unculture	Ogp663 xanthomonas	Ofzex4 orvza sativ	OBgxw3 arabidopsis	O6d9t1 erwinia car	Bac99531 orvza sat	Bac99402 orvza sat	P33308 saccharomyc	Aas56748 saccharom	Ogrvi7 orvza sativ	007920 bacillus su
облахз	Q6JGY1	AAS57675	AAS57683	QBP663	Q6ZCX4	Q8GXW3	Q6D9T1	BAC99531	BAC99402	CSE2 YEAST	AAS56748	Q8RYI7	AZLB_BACSU
8	~	N	7	~	7	~	~	~	~	н	7	~	н
108	108	108	108	130	148	148	148	148	148	149	149	155	157
12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8	12.8
9	9	ø	9	9	9	9	9	9	9	9	9	9	9
32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

KESULT NRG3 M ID N	RESULT I NRG3 MOUSE ID NRG3 MOUSE AC 035181;	ANDAR	, 0	PRT;	713 /	AA.		
	16-OCT-2001 (Rel. 40, Creat 16-OCT-2001 (Rel. 40, Last 05-JUL-2004 (Rel. 44, Last Pro-neurequlin-3 precursor	(Rel. 40, (Rel. 40, I (Rel. 40, I (Rel. 44, I in-3 precu		ed) sequence update) annotation update) (Pro-NRG3) (Contai	ipdate 1 upda 10or	date) update) (Contains: Newreculin-3	reculjin-3 (NDG	
DE UE	3)]. Name-Nrc3.	ı						
SO	Mus musculus (Mouse)	(Mouse).						
000	Eukaryota, Metazoa, Mammalia, Eutheria.		Chordata;		a; Ve	ertebrata;	Craniata, Vertebrata, Euteleostomi,	
N N	NCBI_TaxID=10090;	3	tenre d		ria Cili	; Muitade;	octuloguachi; mullode; mullode; mus.	
RP	SEQUENCE FROM	FROM N.A.						
Z Z	Tissue=Brain; MEDLINE=97420720; PubMed=9275162;	; 0720: РирМе	3d=9275	162.				
RA	Zhang D., Sliwkowski M.X., Mark M., Frantz G.,	iwkowski M.	X., Ma	rk M., F	rantz	G., Akita	R., Sun Y.,	
RA	Hillan K., Crowley C., Brush J., Godowski P.J., "Neureonlin-1 (NRG1): a nowel neural tissus-cariobod	rowley C.,	Brush	J., Godo	wski	P.J.;	40	
RT	binds and ac	tivates Erb	DB4.";	The state of	100	ים בווד דרוופת	היסרבדוו	
R.	Proc. Natl.	Acad. Sci.	U.S.A.	94:9562	-9567	(1997).		
38		Fonction: Direct ilgand for the Ekbb4 Binding results in ligand-stimulated t	ligand Ligand	or the E -stimula	ted t	cyrosine k vrosine nh	tyrosine kinase receptor. tyrosine phosphorylation a	. פ
23	activation of	on of the r	recepto	the receptor. Does not	not h	bind to the		
90	-!- SUBCELLU	EKBB2 OF ERBB3 receptors. SUBCELLULAR LOCATION: Exi	ptors.	מרמ ממ	1	EKBB2 Or ERBB3 receptors. SUBCELLULAR LOCATION: Exists as an type I membrane protein	orotoin on	C n
ט	a proteo	proteolytically released soluble	elease	dulos b	e gro	wth factor		3
ខ្លួ	membrane -!- TISSUE SI	membrane-bound form does not TISSUE SPECIFICITY: Expressed	does Expre	not seem ssed in	to b	does not seem to be active (I Expressed in sympathetic, mot	(By similarity)	}
ยเ			•	,	•			,
មួស	-:- DEVELOPMI detected	DEVELOPMENTAL STAGE: Detected as early as 11 detected mainly in the nervous system at 16	: Dete	cted as	early	as 11 dpc.	dpc. At 13 dpc dpc detected in the	0
נטו	brain, si	brain, spinal cord,		ninal, v	estib	ular-cochle	trigeminal, vestibular-cochlear, and spinal	דוע
20		In adults,	expre	ssed in	spina	l cord, and	numerous brai	п
ပ္ပင္	-!- DOMAIN: The	The cytopla	smic d	omain ma	y be	DOMAIN: The cytoplasmic domain may be involved in the	Ä,	ជួ
308	proteoly	protective processing	ing in	involves i	ocess nitia	initial intracellular	ition of the Lular domain	
38	dimerizat -!- DOMAIN: E	dimerization (By similarity). DOMAIN: ERBB receptor binding is	milari or bin	cy). ding is	elici	elicited entirely by the	v by the EGE-like	
55	-	domain (By similarity).	ty).	}				
មួ	-i- FIM: Fror external	FIM: Froteolytic cleavage close to external face leads to the release	eavage to th	close t ereleas	o the e of	: plasma memb the soluble	FIM: Froteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor	
c) c)	form (By -!- PTM: Exte	(By similarity). Extensive alveosvlation precedes the	osvlati	ממים מס	0			
υ	simil	:y) .	7))		CTCA CARG	ξ <u>α</u>)
888	-!- SIMILARITY: -!- SIMILARITY:	<pre>rY: Belongs to the neu rY: Contains 1 EGF-lik</pre>	to the	the neuregulin family EGF-like domain.	ulin omain	family.		
8881	This SWISS-PROT entry is between the Swiss Instit	OT entry is copyric Swiss Institute of	s copy	copyright. It is produ	t is forma	. It is produced th oinformatics and t	It is produced through a collaboration nformatics and the EMBL outstation -	oration ation -
U	the European Bioinformatics Institute.	Bioinforma	tics II	stitute		There are no	restrictions on	on its

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DISULFID
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Q74FY8;
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Matches
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AC B
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

TISSUE=Fetal brain;

WEDLINE=97420720; PubMed=9275162;

Zhang D., Sliwkowski M.X., Mark M., Frantz G., Akita R., Sun Y.,

Zhang D., Sliwkowski M.X., Godowski P.J.;

Hillan K., Crowley C., Brush J., Godowski P.J.;

Hillan K., Crowley C., Brush J., Godowski P.J.;

Proc. Natl. Acad. Sci. U.S.A. 94:9562-9567(1997).

-! FROTION: Direct Ligand for the REB14 tyrosine kinase receptor.

-! Bindring results in ligand-stimulated tyrosine phosphorylation and activation of the receptor. Does not bind to the EGF receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                          Pfam; PFVZ1D0; NCALCONTENT TO PROSITE; PSO1022; BGF 1; 1.
PROSITE; PSO1186; EGF 2; 1.
PROSITE; PSS0026; EGF 3; 1.
EGF-like domain; Growth factor; Multigene family; Transmembrane.
EGF-like domain; Growth factor; Multigene family; Transmembrane.
CHAIN 1 713 Pro-neuregulin-3, membrane-bound form.
1 361 Neuregulin-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Pro-neuregulin-3 precursor (Pro-NRG3) [Contains: Neuregulin-3 (NRG-
                                                                                                                                                                                                                       Extracellular (Potential).
Internal signal sequence (Potential).
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              288 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 HFKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                           Length 713;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                   similarity.
similarity.
9F7D1D5E7FC8DCF0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           Score 47; DB 1; I
Pred. No. 5.3e-43;
                                                                                          GO; GO:0005515; F:protein binding; IPI.
GO; GO:0007243; P:protein kinase cascade; IDA.
GO; GO:0007242; BGF 2.
InterPro; IPR000422; BGF 1:
InterPro; IPR002154; Neuregulin.
PF00008; BGF; 1.
Pfam; PF00008; BGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          720 AA.
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                           similarity.
                                                                                                                                                                                                                                                          Thr-rich
                                                                                                                                                                                                                                                                             Poly-Ala.
Poly-Ala.
Poly-Thr.
Poly-Ala.
Poly-Ala.
Poly-Ala.
Poly-Ser.
Poly similar
By similar
By similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                         77369 MW;
                                                    EMBL; AF010130; AAB70914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                             100.08;
                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Watches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                        HSSP, P01133; 1JL9.
MGD; MGI:1097165; Nrg3.
                                                                                                                                                                                                                                                                              21
34
135
253
263
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                                                                                                                                                                                                                             362
383
713
287
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                                                                PIR; T44447; T44447.
                                                                                                                                                                                                                                                                                                                                                               321
713 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                 384
105
288
13
26
127
250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=NRG3;
                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                        TRANSMEM
                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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NRG3_HUMAN
                                                                                                                                                                                                                                                             DOMAIN
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ERBEZ OF ERBES receptors.

--- SUBCELDULAR LOCATION: Exists as an type I membrane protein and as a proteolytically released soluble growth factor form. The membrane-bound form does not seem to be active (By similarity).

--- TISSUE SPECIFICITY: Highly expressed in most regions of the brain with the exception of corpus callosum. Expressed at lower level in testis. Not detected in heart, placenta, lung, liver, skeletal muscle, kidney, pancreas, spleen, thymus, prostate, ovary, small intestine, colon and peripheral blood leukocytes.

--- DOMAIN: The cytoplasmic domain may be involved in the regulation of the proteolytic processing. Regulation of the proteolytic processing involves initial intracellular domain dimerization (By similarity).

--- DOMAIN: ERBE receptor binding is elicited entirely by the EGF-like domain (By similarity).

--- PTM: Froteolytic cleavage close to the plasma membrane on the external face leads to the release of the soluble growth factor form (By similarity).

--- PTM: Extensive glycosylation precedes the proteolytic cleavage (By similarity).
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0
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GO; GC:0005887; C:integral to plasma membrane; NAS.
GO; GO:0005887; C:integral to plasma membrane; NAS.
GO; GO:0008083; F:growth factor activity; NAS.
GO; GO:0001259; F:transmembrane receptor protein tyrosine kin. . .; NAS.
GO; GO:0001770; P:transmembrane receptor protein tyrosine kin. . .; NAS.
InterPro; IPR006704; BGF_2.
InterPro; IPR006209; BGF_1ke.
InterPro; IPR006210; IBGF_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neuregulin-3.
Extracellular (Potential).
Internal signal sequence (Potential).
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286 HFKPCKDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 47; DB 1; Length 720; 100.0%; Pred. No. 5.3e-43; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HEKPCRDKDLAYCLNDGECFVIETLTGSHKHCRCKEGYQGVRCDQFL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A4D6F10DDB95A693 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: Belongs to the neuregulin family.
-i- SIMILARITY: Contains 1 EGF-like domain.
HSSP, POLI33; 1JL19.
Genew, HGNC:7999; NRG3.
MIM; 605533; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            By similarity.
By similarity.
By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polý-Ala.
Poly-Ala.
Poly-Thr.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Poly-Ala.
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360
381
720
2285
329
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34
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260
265
304
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319
720 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity).
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382
105
286
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TRANSMEM
DOMAIN
DOMAIN
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Gaps

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Indels

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SEQUENCE FROM N.A.
MEDLINE=90040717; PubMed=2530355;
Auer J., Spicker G., Boeck A.,
"Organization and structure of the Methanococcus transcriptional unit homologous to the Escherichia coli 'spectinomycin operon'.
Implications for the evolutionary relationship of 70 S and 80 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "J. Mol. Biol. 209:21-36(1989).

-!- FUNCTION: This is 1 of the proteins that binds and probably mediates the attachment of the 5S RNA into the large ribosomal subunit, where it forms part of the central protuberance. In the 70S ribosome it contacts protein $13 of the 30S subunit (bridge Blb), connecting the 2 subunits; this bridge is implicated in subunit movement. May contact the P site tRNA, the 5S rRNA and some of its associated proteins might help stabilize positioning
                                                                                                                                                                                                                                                                                                                 Beta vulgaris (Sugar beet).
Makaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophylales; Amaranthaceae; Beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schneider K., Weisshaar B., Borchardt D.C., Salamini F., "SNP frequency and allelic haplotype structure of Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mol. Breed. 8:63-74(2001).
EMBL; AF295647; AALO4443.1; -.
GO; GO:0004047; F:aminomethyltransferase activity; IEA.
InterPro; IPR006222; GCV_T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AA; 13979 MW; 19E599611A064040 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archaea; Euryarchaeota; Methanococci; Methanococcales;
                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
it T (Fragment).
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. 13;
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01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
50S ribosomal protein LSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.9%; Scor.
100.0%; Pred. No. 10.
                                                                                                                                                                                   127 AA
          Mismatches
                                                                                                                                                                                                                  (TrEMBLrel. 19, Created)
                                                                                                                                                                                 PRT;
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0
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                                                                                                                                                                                                                01-DEC-2001 (TrEMBLRE1. 19, Cr
01-DEC-2001 (TrEMBLRE1. 19, La
01-OCT-2003 (TrEMBLRE1. 25, La
Glycine decarboxylase subunit
      7; Conservative
                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
nes 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=rpl5p;
Methanococcus vannielii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01571; GCV_T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 CRDKDLA 103
                                          17 GECEVIE 23
                                                                                65 GECFVIE 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 CRDKDLA 11
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=161934;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed genes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=2187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ribosomes.";
                                                                                                                                                                                                                                                                                             Name=gdt;
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P14029;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                               0947L6
      Matches
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                                                                                                                                           RESULT 5
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ID 09
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                                                                                                                                                                             STRAIN-PCA / ATCC 51573;
STRAIN-PCA / ATCC 51573;
STRAIN-PCA / ATCC 51573;
STRAIN-PCA / ATCC 51573;
STRAIN-PCA / DATCC 51573;
STRAIN-PCA / DATCC 51573;
Mothe B.A., Nelson K.E., Eisen J.A., Paulsen I.T., Nelson W.C., Heidelberg J.F., Wu D., Wu W., Ward N.L., Beanan M.J., Dodson R.J., Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S., Gwinn M.L., Kolonay J.F., Shalivan S.A., Haft D.H., Selengut J., Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A., Weidman J.F., Khouri H.M., Feldblyum T.V., Utterback T.R., Van Aken S.E., Lovley D.R., Fraser C.M.;
"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

STRAIN=PCA / ATCC 51573;

STRAIN=PCA / ATCC 51574;

STRAIN=PCA / ATCC 51574;

STRAIN=PCA / ATCC 5174;

Madupu R., Brinkac L.M., Daugherty S.C., DeBoy R.T., Durkin A.S.,

Madupu R., Rolnay J.F., Sullivan S.A., Haft D.H., Selengut J.,

Davidsen T.M., Zafar N., White O., Tran B., Romero C., Forberger H.A.,

Weidman J., Khouri H.M., Feldblyum T.V., Utterback T.R.,

Van Aken S.E., Lovley D.R., Fraser C.M.;

"Genome of Geobacter sulfurreducens: metal reduction in subsurface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                      Geobacter sulfurreducens.
Bacteria, Proteobacteria, Deltaproteobacteria, Desulfuromonadales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Geobacter sulfurreducens.
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales;
Geobacteraceae; Geobacter.
VCNI_TaxID=35554;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7704 MW; 9C0D6C2C84E02AD9 CRC64;
            05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 AA; 7704 MW; 9C0D6C2C84E02AD9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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Pred. No.
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Pred. No.
Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE017180; AAR33796.1; -.
TIGR; GSU0464; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 302:1967-1969(2003).
EMBL; AE017208; AAR33796.1; -.
TIGR; GSU0464; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; S
100.0%;
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                                                                                                                             Geobacteraceae, Geobacter.
NCBI_TaxID=35554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGR; GSU0464; -.
InterPro; IPR002942; S4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01479; S4; 1.
SMART; SM00363; S4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50889; S4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 GECFVIE 23
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                                                S4 domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 AA;
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Matches 7; Conserv
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Best Local Similarity
                                                                      ORFNames=GSU0464;
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                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                       Gaps
of ribosome-bound tRNAs (By similarity).
SUBUNIT: Part of the 50S ribosomal subunit; contacts the 5S rRNA and probably tRNA. Forms a bridge to the 30S subunit in the 70S ribosome (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUN-2003 (TrEMBLrel. 24, Created)
01-UUN-2003 (TrEMBLrel. 24, Last sequence update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
01-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Putative gland protein G11A06.
Heterodera glycines (Soybean cyst nematode).
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Heteroderiaa; Heteroderiaa; Heteroderiaa; Heteroderiaa; Heteroderiaa; Norbi_TaxID=51029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=22787455; PubMed=12906116;
Gao B., Allen R., Maier T., Davis E.L., Baum T.J., Hussey R.S.;
"The parasitome of the phytonematode Heterodera glycines.";
Mol. Plant Microbe Interact. 16:720-726(2003).
                                                                                                                                                                                  R HSSP, P41201, IMJI.

R HSSP, P41201, IMJI.

R HAMAR, ME 01333, -; 1.

R HAMAR, ME 01333, -; 1.

R InterPro; IRR002135; Ribosomal_L5.

R InterPro; IRR00235; Ribosomal_L5. 1.

R Pfam; PF001281; Ribosomal_L5, 1.

R ProDom; P00101434; Ribosomal_L5 mit.

DR ProDom; P0013434; Ribosomal_L5 mit; 1.

DR ProDom; P0013434; Ribosomal_L5 mit; 1.

R Ribosomal protein; RNA-binding; RNA-binding.

KW Ribosomal protein; RNA-binding; RNA-binding.
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                                              SIMILARITY: Belongs to the L5P family of ribosomal proteins
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                Length 181,
                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF500015; AAP30754.1; -.
SEQUENCE 186 AA; 19221 MW; AB01E9CF13699E34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                           14.9%; Sco...
100.0%; Pred. No. ...
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                EMBL; X16720; CAA34693.1; -. PIR; S05617; R5MX5.
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Best Local Similarity 100.
Matches 7; Conservative
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Best Local Similarity
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01-OCT-2002
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Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M., Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahl B.B., Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M., Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
NCBI_TaxID=180454;
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

Hypothetical protein OSJNBa0078001.15.

ORFNames=OSJNBa0078001.15;

ORFyza sativa (japonica cultivar-group).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anopheles Genome Sequencing Consortium, Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the Rice Chromosome 10 Sequencing Consortium; "In-depth view of structure, activity, and evolution of rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC079888; AAM93694.1; -.
EMBL; AE017109; AAP54466.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 368;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 368 AA; 40524 MW; 2595A70161DE151B CRC64;
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01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gramene; Q8LNG9; -.
InterPro; IPR008975; Viral_cap_coat.
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InterPro; IPR003341; DUF139.
InterPro; IPR006209; EGF_like.
Pfam; PF02363; C_triplex; 7.
PROSITE; PS01186; EGF_2; 3.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 300:1566-1569(2003).
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nes 7; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                               NCBI_TaxID=39947;
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Matches

RESULT 10

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                            01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine cleavage_system T protein) (GCVT).
                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids,
lamiids, Solanales, Solanaceae, Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycine.

-I- CATALYTIC ACTIVITY: Protein-S-aminomethyldihydrolipoyllysine +
tetrahydrofolate = protein-dihydrolipoyllysine + 5,10-
methylenetetrahydrofolate + NH(3).

-I- SUBNIT: The glycine cleavage system is composed of four proteins:
P, T, L and H.
                                                                                                                                                                                                                                                                                                                                                                           Kopriva S., Bauwe H., "T-protein of glycine decarboxylase from Solanum tuberosum."; Plant Physiol, 104:1079-1080(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Similar to sp|P48015 Saccharomyces cerevisiae YDR019c GCV1 glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORFNames=YALIOF02849g,
Yarrowia lipolytica (Candida lipolytica).
Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Dipodascaceae, Yarrowia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR006223; GcvT.
InterPro; IPR006222; GcvT.
Pfam; PF0157; Gcv T; 1.
TIGRFAMs; TIGR00528; gcvT; 1.
Aminotransferase; Mitochondrion; Transferase; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mitochondrion (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aminomethyltransferase. F52F4A13D70E33AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.9%; Scor.
100.0%; Pred. No. 50.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SÚBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: Belongs to the gcvT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last seq
01-OCT-2004 (TrEMBLrel. 28, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94218396; PubMed=8165246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44276 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z25862; CAA81081.1; -. PIR; S59948; S59948.
                                                                                                                                                                       Solanum tuberosum (Potato)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
7, Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                150 CRDKDLA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30 4
406 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5 CRDKDLA 11
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                          lamiids; Solanale
NCBI_TaxID=4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=4952;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    decarboxylase
                                                                                                                                                                                                                                                                                                                                TISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q6C340;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q6C340
           ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                           10-0CT-2003 (Rel. 42, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA Seq. 13:179-183 (2002).

-!- FUNCTION: The glycine cleavage system catalyzes the degradation of glycine (Bp similarity).

-!- CATALYTIC ACTIVITY: Protein-6-aminomethyldihydrolipoyllysine + tetrahydrofolate = protein-6-inpoyllysine + 5,10-methylenetetrahydrofolate + NH(3).

-!- CBUNIT: The glycine cleavage system is composed of four proteins: P, T, L and H (By similarity).

-!- SUBUNIT: NHORATION: Mitochondrial (By similarity).
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=129S6/SVBvTac;
MEDLINE=22375501; PubMed=12487019;
Backofen B., Leeb T.;
"Genomic organization of the murine aminomethyltransferase gene
                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; iranous...;
Pfam, PF01571; GCT; 1.7
TIGREAMS, TIGRO528; gcvT; 1.
Aminotransferase; Mitcchondrion; Transferase; Transit pepti
TRANSIT 1 28 Mitcohondrion (By similarity).
Aminomethyltransferase.
403 Aminomethyltransferase.
                                                  Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.9%; Score 7; DB 1; Length 403; 100.0%; Pred. No. 35; tive 0; Mismatches 0; Indels
                                                                                             0; Indels
43118 MW; 9629287CAB405B77 CRC64;
                                             DB 2;
                       14.9%; Scorr
100.0%; Pred. No. cr
10.0%; Mismatches
                                                                                                                                                                                                                                                                                                      403 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                       cleavage system T protein) (GCVT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AJ437692; CAD26917.1; -.
                                                                                                                                                                                                                                                                                                                                               (Rel. 42, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro, IPR006223; GCvT.
InterPro, IPR006222; GCv_T
                                                                                          Conservative
                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                              207 CRCKEGY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                      CRCKEGY 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRDKDLA 154
401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRDKDLA 11
                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                            10-OCT-2003
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GCST_SOLTU
ID GCST_SOLTU
                                                                                                                                                                                                                                                                                               GCST_MOUSE
Q8CFA2;
                                                                                                                                   32
SEQUENCE
                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
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ID GCST_MOUSE

OF ORCEAN

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or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Name=GDCST
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                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                               150
                                                                                                                                                                           Query Match
                                                                                                                     TRANSIT
                                                                                                                                                                                                                                                                                                                                                P49363;
                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                               Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
A Dujon B., Sherman D., Fischer G., Neuveglise C., Talla B.,
Infontaine I., de Montigny J., Marck C., Neuveglise C., Talla B.,
A Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
A Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykaaten C.,
A Boisrame A., Boyer J., Cattolico L., Confanioleri F., de Daruvar A.,
A Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
A Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
A Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
A Swennene D., Tekata F., Wesolowski-Louvel M., Westhof E., Wirth B.,
A Caniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
A Wincker P., Souciet J.L.,
I "Genome evolution in yeasts.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycine.
CARALYTIC ACTIVITY: Protein-S-aminomethyldihydrolipoyllysine +
CARALYATCA CALOLATE = protein-dihydrolipoyllysine + 5,10-
methylenetetrahydrofolate + NH(3).
SUBUNIT: The glycine cleavage system is composed of four proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-UUL-1998 (Rel. 36, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
01-007-2004 (Rel. 45, Last annotation update)
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine cleavage system T protein) (GCVT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Tageteae; Flaveria.
NCBI_TaxID=35877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nan Q., Chu C.-C., Bauwe H.;
"The GDCST gene encoding T-protein of the glycine cleavage system in the C3-C4 intermediate plant Flaveria anomala.";
(er) Plant Gene Register PGR98-006.
                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: The glycine cleavage system catalyzes the degradation
                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                              Genoscope; Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          EMBL; CR382132; CAG77727.1; -.
SEQUENCE 406 AA; 43990 MW; C4FA50AB6C55857B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 5;
                                                                                                                                                                                                                                                                                                                                                                              14.9%; Score 7; DB 2; 100.0%; Pred. No. 36; iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SÜBCELLULAR LOCATION: Mitochondrial.
-!- SIMILARITY: Belongs to the gcvT family.
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                       Nature 430:35-44(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  153 CRDKDLA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                         5 CRDKDLA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P, T, L and H.
                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Flaveria anomala.
                                                                                                                                                                                                                                                                                                  STRAIN=CLIB99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCST FLAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=GDCST
                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
GCST_FLAAN
                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kopriva S., Turner S.R., Rawsthorne S., Bauwe H.;
"T-protein of the glycine decarboxylase multienzyme complex: evidence for partial similarity to formyltetrahydrofolate synthetase.";
Plant Mol. Biol. 27:1215-1220(1995).
- FUNCTION: The glycine cleavage system catalyzes the degradation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine cleavage system T protein) (GCVT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Flaveria pringlei.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Tageteae; Flaveria.
                                                                                                                                                                                                                                                                                      ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide.
                                                          Pfam; PF01571; GCV T: 1.
TIGRFAMS; TIGR00528; gcvT; 1.
Aminotransferase; Mitochondrion; Transferase; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 407;
                                                                                                                                                                                                                                                                                      0; Indels
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44353 MW; 8B87F7EBE679F7C0 CRC64;
                                                                                                                                                                                       7F1BE2896CDD1A59 CRC64;
                                                                                                                                         Mitochondrion (Potential)
Aminomethyltransferase.
                                                                                                                                                                                                                                     14.9%; Score 7; DB 1;
100.0%; Pred. No. 36;
iive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               407 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95284371; PubMed=7766903;
                                                                                                                                                                                          407 AA; 44279 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z25858; CAA81077.1; -.
PIR; S56660; S56660.
                 InterPro; IPR006223; GCVT.
InterPro; IPR006222; GCV_T.
EMBL; Z71184; CAA94902.1;
                                                                                                                                                                                                                                                                       Local Similarity 100.
Les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                        407
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                                                                                                                                                                                                                                                                                                                                           5 CRDKDLA 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Aminomethyltransferase, mitochondrial precursor (EC 2.1.2.10) (Glycine oleavage system T protein) (GCVT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Flaveria trinervia (Clustered yellowtops).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Asteroideae; Tageteae; Flaveria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glycine.
-!- CATALYTIC ACTIVITY: Protein-S-aminomethyldihydrolipoyllysine +
tetrahydrofolate = protein-dihydrolipoyllysine + 5,10-
methylenetetrahydrofolate + NH(3).
-!- SUBUNIT: The glycine cleavage system is composed of four proteins:
P. T. L and H.
-!- SUBCELLUIAR LOCATION: Mitochondrial.
-!- SIMILARITY: Belongs to the gcvT family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SECUENCE FROM N.A.

TISSUB=Leaf;
Cossu R., Bauwe H.;

"The GDGS" and encoding T-protein of the glycine cleavage system in the C4 plant Plaveria tringfyia.";
(er) Plant Gene Register PGR98-007.

-!- FUNCTION: The glycine cleavage system catalyzes the degradation of
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; 299769; CAB16>1...

EMBL; 299769; CAB16>1...

InterPro; IPR006223; GCvT.

R InterPro; IPR006222; GCvT.

R Ffam; PF01571; GCvT 1...

DR TIGRFAMS; TIGR00528; gcvT; 1...

TIGRFAMS; TIGR00528; gcvT; 1...

Mitochondrion (Potential).

TOWN Aminotransferase.

TOWN Aminomethyltransferase.

TOWN Aminomethyltransferase.

TOWN Aminomethyltransferase.

Town 407;
                                                                                ·,
          Length 407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.9%; Score 7; DB 1; Length 407; llarity 100.0%; Pred. No. 36; Conservative 0; Mismatches 0; Indels
                                                                         0; Indels
          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                        407 AA.
Query Match
14.9%; Score 7; DB 1.
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                     150 CRDKDĽA 156
                                                                                                                                          5 CRDKDLA 11
                                                                                                                                                                                                                                                                                                                                                                                        FLATR
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Best Local S
                                                                                                                                                                                                                                                                                                           RESULT 15

GOST FLATR

AC 023936.
DT 15-JUL.
DT 15-JUL.
DE Cleaves:
GN Name=Gl
OC Spermal/
OC Campan

OC Campan

OC Campan

OC Spermal/
CC Campan

CC Spermal/
CC 
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Gaps

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Search completed: November 2, 2004, 13:45:29 Job time : 195 secs

150 CRDKDLA 156

5 CRDKDLA 11 Similarity 7; Conserv

> 8 qq

Matches